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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                          870385 seqs, 699768693 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                            Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq: /cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*

ptodata/2/pubpna/US09_NEW_PUB.seq: /ptodata/2/pubpna/US09_PUBCOMB.seq

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq

SUMMARIES

Description	Sequence 1, Appli	-	1, 2	H		Sequence 26, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 2360, Ap	Sequence 1, Appli	Sequence 3, Appli		11,	-	Ā	2	Sequence 14, Appl		Sequence 14, Appl
Desc	Sed	Sec	Sec	Se	Sec	Sec	Sec	SS	Se	Se	Sec	Sec	Sec	S	Sec	Se	Sec	Sec	Sec
ID	US-09-898-234-1	US-09-899-429A-1	US-09-792-356-1	US-09-899-422-1	US-09-898-234-16	US-09-899-429A-26	US-09-792-356-16	US-09-899-422-16	US-09-880-107-2360	US-10-120-397-1	US-10-252-408-3	US-09-898-234-11	US-09-792-356-11	US-09-899-422-11	US-09-899-429A-21	US-09-917-800A-1601	US-09-898-234-14	US-09-899-429A-24	US-09-792-356-14
DB	6	6	6	10	σ	σ	σ	10	10	12	0	6	6	10	6	10	σ	σ	σ
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Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.66	99.9	99.6	82.0	82.0	82.0	81.7	54.3	53.8	53.8	53.8
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10 US-09-899-422-14 10 US-09-970-532-1 9 US-09-899-4228-7 9 US-09-899-4228-7 9 US-09-899-4228-13 9 US-09-899-4228-13 9 US-09-899-4238-17 9 US-09-899-4238-17 10 US-09-756-186-7 9 US-09-756-186-7 10 US-09-756-186-5 9 US-09-898-234-3 9 US-09-899-4238-3 10 US-09-911-904-129 10 US-09-976-186-3 10 US-09-976-889-386-11
2173 2440 6633 603 603 579 570 1301 1301 1483 4883 4883 4483 4483 1202 1202 543 570
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ALIGNMENTS

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1 Sequence 1, Application US/09896234
1 Sequence 1, Application US/09896234
1 Sequence 1, Application US/09896234
1 Sequence 1, Application Model
2 SepticANT Hammler, Adoubt
3 APPLICANT HAMMLER, Adoubt
4 APPLICANT HAMMLER, Adoubt
5 APPLICANT Stratowa, Christian
7 TILLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAs Coding for TILLE REFERENCE: 98.385-I
CURRENT FILING DATE: 2000-03-15
PRIOR PELICATION NUMBER: 06/355,98
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1955-02-03
PRIOR FILING DATE: 1955-02-03
PRIOR FILING DATE: 1953-01-03
PRIOR PILING DATE: 1950-04-03
PRIOR PRIOR PILING POTION OF THE PIPORMATION: Extracellular proteases following secretion: 100AMI/RET PIPORMATION: POTION OF THE PIP
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GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG 1020
                         CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCG
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APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingtid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REPERSUCE: 98-38-3
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT FILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1995-01-11-17
PRIOR PILING DATE: 1993-11-17
PRIOR PILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR PILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR PILING DATE: 1993-11-17
PRIOR PILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR PILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1900-04-20
PRIOR FILING DATE: 1900-04-20
PRIOR FILING DATE: 1900-04-20
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CTHER INFORMATION: portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion NAME/KEX: misc_feature
ICCATION: (606)..(633)
CTHER INFORMATION: portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion US-09-899-429A-1
                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
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LOCATION: (1)..(1365)
NAME/KEY: $19_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
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                                    1368;
OTHER INFORMATION: extracellular proteases following secretion
                                    Length
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                                 100.0%; Score 1368;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                   Query Match
Best Local Similarity 100.
Matches 1368; Conservative
  ; OTHER INFORU
US-09-898-234-1
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Sequence 1, Application US/09792356
Publication No. US20020183485A1
GENERAL INPORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauter, Adolph
APPLICANT: Hauter, Adolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-10-02
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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                      GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCCCTAGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(87)

NAME/KEY: misc_feature

LOCATION: (88)..(120)

OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.

NAME/KEY: misc_feature

LOCATION: (606)..(633)

OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.

US-09-792-356-1
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NAME/KEY: sig_peptide
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ORGANISM: HOMO
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Qy 1081 GCCGTGGTGGAACGTCCCCGTTGCGTGGAAGAATTCGTGCGCGCCTAGGGTG 1140 Db 1081 GCCGTGGTGGAACGTGGCTGGAAGGAATTCGTGCGCGCCTAGGGTG 1141 Db 1141 AGCGACCACGAATCGGTGGACTGCAGAGGAATTCGTGCGCGCGC	RESULT 4 US-09-899-422-1 Sequence 1, Application US/09899422 Fatent No. US-20020090676A1 GENERAL INFORMATION: APPLICANT: Hamptmann, Rudolph APPLICANT: Hammler, Adolph APPLICANT: Hammler, Adolph APPLICANT: Stratowa, Christian TITLE OF INVENTION: THE Receptors, TNF Binding Proteins and DNAS Coding for TITLE OF INVENTION: Them FILE REFERENCE: 98, 385-4 CURRENT APPLICATION NUMBER: US/09/699,422 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: 09/525,998 FRIOR APPLICATION NUMBER: 08/383,676 FRIOR FILING DATE: 1995-00-1 PRIOR FILING DATE: 1995-00-1 PRIOR FILING DATE: 1995-00-1 PRIOR PRIOR APPLICATION NUMBER: 08/383,676 FRIOR FILING DATE: 1995-00-1	PRIOR APPLICATION NUMBER: 07/821,750 PRIOR FILING DATE: 1992-01-02 PRIOR FILING DATE: 1990-04-20 PRIOR FILING DATE: 1990-04-20 STORING SEQ ID NOS: 87 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 1368 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (1)(1368) NAME/KEY: sig_peptide LOCATION: (1)(87) NAME/KEY: misc_feature LOCATION: (1)(87) NAME/KEY: misc_feature LOCATION: (1)(87) COTHER INFORMATION: Portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion.	NAME/KEY: misc_feature ; LOCATION: (606)(633) ; OTHER INFORMATION: POTION of TNF-BP pro protein cleaved by ; OTHER INFORMATION: extracellular proteases following secretion. US-09-899-422-1 Query Match Best Local Similarity 100.0%; Score 1368; DB 10; Length 1368; Best Local Similarity 100.0%; Pred. No. 0; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGGGCCTCTCCACGGTGCTGACCTGCTGCTGCTGCTGCTGTGTG 60 International Conservational Conse
ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG	301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGGGGCTCAGTGGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	Oy 601 AATGTTAAGGGCACTGAGGCACCACAGTGCTGTTGCCCTGGTCATTTTTTT 660 Db 601 AATGTTAAGGCACTGAGGACTCAGTGCTGTTGCCCTGGTCATTTTTTTT	0y CCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGACGGTGGCACCCCTATCAGGG 960 111111111111111111111111111111111111

		Oy 1141 AGCGACCACGAGATCGGTGGAGCTGCAGAACGGGGGCTGCTGCGGGGGGCGAA 1200	RESULT 5 US-09-808-234-16 Sequence 16, Application US/09898234 Patent No. US/002015112A1 SERURAL INFORMATION: APPLICANT: Hauptmann, Rudolph APPLICANT: Haimler, Adolph TITLE OF INVENTION: Them TITLE OF INVENTION: Them TITLE OF INVENTION: Them CURRENT APPLICATION NUMBER: US/09/808,234 CURRENT APPLICATION NUMBER: US/09/808,234 CURRENT APPLICATION NUMBER: 09/525,998 PRIOR FILING DATE: 2000-03-15 PRIOR APPLICATION NUMBER: 08/383,676 PRIOR FILING DATE: 109/5-02-03 PRIOR FILING DATE: 109/5-02-03 PRIOR FILING DATE: 109/5-02-03 PRIOR FILING DATE: 1993-11-17	FRIOR FILING DATE: 1992-01-02 PRIOR FILING DATE: 1990-04-20 PRIOR FILING DATE: 1990-04-20 NUMBER OF SEQ ID NOS: 87 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 16 LENGTH: 2141 TYPE: DNA NAME/KEY: CDS LOCATION: (213)(1580) COTHER INFORMATION: INFFR2 US-09-898-234-16	Query Match 100.0%; Score 1368; DB 9; Length 2141; Best Local Similarity 100.0%; Pred. No. 0; DB 9; Length 2141; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ArdGGCCTCTCCACGTGCTGCTGCTGCTGGTGCTGTGTGTG 60 Indels 0; Gaps 0; Gaps 0; Qy 513 ArGGCCTCTCCACGTGGTGTTGTTGGTGTGCTCTGGGGGCTGTGTGTG
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QY 1321 CTTTGCGGCCCCGCCGCCCCGCGCCCAGTCTTCTCAGATGA 1368	51 - O II O	APPLICANT: Maurer-Fogy, ingrid APPLICANT: Stratowa, Christian TITLE OF INVENTION: The Receptors, TNE TITLE OF INVENTION: Them FILE REPERENCE: 98-38-3	CURRENT APPLICATION NUMBER: 08/09/899,429A CURRENT FILING DATE: 2001-07-03 PRIOR APPLICATION NUMBER: 09/792,356 PRIOR FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: 08/477,639 PRIOR RILING DATE: 1955-06-07 PRIOR PILING DATE: 08/383,676	•	PRIOR FILING DATE: 1990-0. NUMBER OF SEQ ID NOS: 97 SOFTWARE: Patentin Ver: 2 SEQ ID NO 26 IENGEH: 2141 TYPE: DNA) ORGANISM: Artificial Sequence ; FRATURE: ; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in ; OTHER INFORMATION: 1TNF-R2 ; NAME/KEY: CDS	(213)(1577) A-26	Query Match 100.0%; Score 1368; DB 9; Length 2141; Best Local Similarity 100.0%; Pred. No. 0; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AIGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG	61 273	121 GATAGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTGATTTGCTGTACC 	Oy 181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGGCGGGGGAGGATACGGAC 240	241	301 AGCIGCICCAAAIGCCGAAAGGAAAIGGGICAGGIGGAGAICTCITGCACAGIGGAC	QY . 351 CGGGACACCGTGTGTGCGCAGGAAGAACCAGTACCGGCATTATTGGAAAACCTT 420
241 TGCAGGGAGTGTGAGGGGCTCCTTCACGAAAACCACCTCAGACACACTGCCTC 300 	301 AGCTGCTCCAAATGCCGAAAGGAAATGGCTCAGGTGGACATCTTTTTGCACAGTGGAC 360	CAGGAG	# ## ### #############################	601 AATGTTAAGGGACTGAGGACTCAGGCACCACAGTGCTGTGCCCCTGGTCATTTCTTT 660 [### ### ##############################	GGAACTACTACTAAGCCCTGGCCCAAACCCAAGCTTCAGTCCCACTCCAGGTTCACC 	841 CCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGAAGAGGTGGCACCACCTATCAGGG 960 	961 GCTGACCCCATCCTTGCGACAGCCTCGGCTCCGACCCCATCCCCAACCCCCTTCAGAAG 1020 	1021 IGGGAGGACAGCGCCACAAGCCACAGAGCCTAGACACTGATGACCCGGGACGCTGTAC 1080 	1081 GCCGTGGTGGAAACGTGCCCCGTTGCGCTGGAAGGAATTCGTGCGCGCCCTAGGGCTG 1140 	1141 AGGACCAGGAGATGATGGGCTGGAGCTGCAGAGGGGGCGCTGCCTGGGGGGGG	1201 TACAGCATGCTGGCGCCCCCCCCCCCCCCCCCCCCCCCC	1261 CTGGGACGCGTGCTCCCCCGCACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCG 1320 	

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AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGACTCTCTTGCACAGTGGAC
                        APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: The Receptors, INF Binding Proteins and DNAs Coding
TITLE OF INVENTION: Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
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... OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in CHER INFORMATION: 1TNF-R2
US-09-792-356-16
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; Pred. No. 0;
0; Mismatches
                                                                                      US/09/792,356
                                                                    TILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,3
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 08/183,287
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR PILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
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                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
 Hauptmann, Rudolph
Himmler, Adolph
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SEQ ID NO 16
LENGTH: 2141
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Best Local Similarity 100.
Matches 1368; Conservative
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Sequence 16, Application US/09792356 Publication No. US20020183485A1 GENERAL INFORMATION;

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OTHER INFORMATION: Description of Artificial Sequence: human TNF-R

OTHER INFORMATION: 1TNF-R2
US-09-899-422-16
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100.0%; Score 1368;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR PELING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 16
LENGTH: 2141
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Patent No. US20020090676A1
GENERAL INFORMATION:
APPLICANT: Hampler, Adolph
APPLICANT: Hampler, Adolph
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
CURRENT APPLICATION WUMBER: US/09/899,422
CURRENT APPLICATION NUMBER: 09/525,998
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR APPLICATION NUMBER: 08/383,676
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Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	1 AIGGCCTCTCCACGTGCCTGACCTGCTGCTGCACGTGCTCCTGGAGCTGTTGGTG 60	256 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGCTGCTGGTGTTGGTG 31	OY OCANATATION OF THE STANDARD	121 GATAGTGTGTCCCCAAGGAAATATATCCACCTCAAAATAATGATTGGTGTACC 18	376 GAFAGTGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATGGATTTGCTGTACC 43 181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGCAGGATACGAC 24	OCACAAAGGAACCTACTTGTACAATGACTGTCCAGGGCCGGGGCAGGATACGGA IGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCT 	n 9	Oy 361 CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420	1 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGGG 48	QY 481 AAACAGAACACCGTGTGCACTGCCAGGTTTCTTCTAAGAAAACGAGTGTGTC 540 1 1 1 1 1 1 1 1 1 1	QY 541 TCCTGTAGTAACTGTAGAAAAGCCTGGAGTGCAGGAGTTGTGCCTACCCCAGATTGAG 600	Oy 601 AATGTTAAGGGCACTGAGGCACCCCAGGTGCTGTTGCCCCTGGTCATTTCTTT 660	Qy 661 GGTCTTTGCCTTTCATTGGTTTAATGTATGATGTACCAACGGTGGAAG 720	Qy 721 ICCAAGCICTACICCAITGITGIGGGAAAICGACACCIGAAAAAGAGGGGGAGCITGAA 780	Oy 781 GGAACTACTACTAAGCCCCTGGCCCAAACCCAAGCTTCAGTCCACCTCCAGGCTTCACC 840	Oy 841 CCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTCCACCTCACCTATACC 900	Oy 901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCCGCAGAGGGGGGCTGCCCACCATCAGGGG 960 Db 1156 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGGGGGCACCACCATCAGGGG 1215	Qy 961 GCTGACCCCATCCTTGCGACAGCCCTCGGACCCCATCCCCATCCCCATCCCCTTCAGAG 1020	QY 1021 TGGGAGGACAGGCCCACAAGCCTAGAGCCTAGACACTGATGACCCGGGAGGAGGTGTAC 1021 TGGGACGACACAGAGCCCACAGAGCCTAGAGAGAGAGAGA
		OY 1141 AGGGACCACGAGATGGATGGGCTGCAGCTGCAGACGGGGGCGCTGCCTGC	1327 ACCACCACAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGC	<pre>uy</pre>	Oy 1261 CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGGACATCGAGGAGGCG 1320	Oy 1321 CTTTGCGGCCCGCCCCCCCCGCGCCCAGTCTTCTCAGATGA 1368 	RESULT 10 US-10-120-397-1 ; Sequence 1, Application US/10120397 ; Patent No US/200701423571	GENERAL INFORMATION: APPLICANT: WALLACH, David BRAKEBUSCH, Cord	TITLE OF INVESTION: THE RECEPTOR ACTION MODULATION NUMBER OF SEQUENCES: 8 . CORRESPONDENCE ADDRESSE: ADDRESSES: BROWNY AND NEIMARK CORRESPONDENCE ADDRESSES: CORRESPONDENCE ADDRESSES BROWNY AND NEIMARK	SIGNATE WAShington STATE: D.C. COUNTRY: USA	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC competible COMPUTER: IBM PC competible		FILTING DATE: LT APL 2002 PRIOR APPLICATION: CURKNOWN: PRIOR APPLICATION DATA: FILTING DATE: 03-MAY-1003		TELECOHUNICATION INFORMATION: TELEPRIC 100-628-5197 TELEPRIC 202-628-5197 	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2175 base pairs	STRANDEDINESS: aligned STRANDEDINESS: align	SEQUENCE DESCRIPTION: SEQ ID NO: 1:	Query Match 99.9%; Score 1366.4; DB 12; Length 2175; Best Local Similarity 99.9%; Pred. No. 0;

ATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAGG 		301 AGCTGCTCCAAATGCCGAAAGGGACTCAGGTGGAGTCTCTTCTTGCACAGTGGAC 360 11111111111111111111111111111111111	361 CGGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	481 AAACAGAACACCGTGCCCATGCAGGTTTCTTTCTAAGAAAACGGGTGTGC 540	541 TCCTGTAACTGTAACAAAAACCCTGGGGCGCGCGACGTGTGCCTACCCCGGTTGTG 600 601 AATGTAAGGGCACTGAGACACACACACAGTGTGCCCTGGTCATTTCTT 660 11111111111111111111111111111111111	661 GGTCTTTGCCTTTTATCCTCCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG 720	721 TCCAAGCTCTACTCCATTGTTGGGGAATCGACACTCAAAAAGGGGGGAGCTTGAA 780 781 GGAACTACTACTACAGCCCTGGCCCCAAACCCAAGCTTCAGTCCCAGTCCAGGCTTCACC 840 111111111111111111111111111111111111	841 CCCACCCTGGGCTTCAGTCCCGTGCTCACCTTCACCTCCAGCTCCACCTATACC 900	901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGAGAGAGGTGGCACCACCCTTCAGGGG 960 961 GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCAACCCCTTCAGAAG 1020 961 GCTGACCCTTGCGACAGCCCTCGCTCCGACCCCAACCCCTTCAGAAG 1020 961 GCTGACCCCTTGCGACAGCCCTCGCTCCGACCCCTTCAGAAG 1020	GGGAGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCGGGGACGCTGTAC 108	1091 GCCGTGGTGGTGCCCCCCTTGCGTGGAAGAATTCGTGCGCGCCTAGGCTG 1140 1081 GCCGTGGTGGTGCCCCCCGTTGCGTGGAATTCGTGCGGCGCCTAGGCTG 1140
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Qy 1081 GCCGTGGTGGAGAGGTGCCCCGTTGCGCTGGAGGAATTCGTGGGCCCTAGGGCTG 1140 Db 111111111111111111111111111111111111		Oy 1321 CTTTGCGGCCCGCCCTCCGCCCCCCGGCCCCAGTCTTCTCAGATGA 1368	S-10-252-408-3 Sequence 3, Application US/10252408 Publication No. US20030082736A1 GENERAL INFORMATION:	FILE REFERENCE: A-71592 CURRENT APPLICATION NUMBER: US/10/252,408 CURRENT FILING DATE: 2002-09-24 PRIOR APPLICATION NUMBER: US/08/406,824 PRIOR PILING DATE: 1995-03-20 PRIOR PILING DATE: 1995-03-20		FRIOR FILLING DATE: 1989-10-13 FRIOR APPLICATION NUMBER: US 07/405,370 FRIOR FILLING DATE: 1989-09-11 FRIOR APPLICATION NUMBER: US 07/403,241 FRIOR FILLING DATE: 1989-09-05 NUMBER OF SEQ ID NOS: 29	တ		COTHER INFORMATION: FEATURE: NAME/KEY: s1g_peptide COTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION: CS-10-252-408-3	Query Match 99.6%; Score 1363.2; DB 9; Length 1368; Best Local Similarity 99.8%; Pred. No. 0; Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	0y 1 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGCTCCTGGAGCTGTTGGTG 60

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Publication No. US20020183485A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Haumler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratcowa, Christian
TITLE OF INVENTION: THE Receptors, TNF Bir
TITLE OF INVENTION: Them
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Patent No. US20020155112A1

GENERAL INFORMATION:

APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Matter-Fogy, Ingrid
APPLICANT: Matter-Fogy, Ingrid
APPLICANT: Matter-Fogy, Ingrid
APPLICANT: Matter-Fogy, Ingrid
APPLICANT: MATTER CENTRAL Them
TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-1
CURRENT APPLICATION NUMBER: US/09/898,234
CURRENT FILING DATE: 2001-07-03
PRIOR FILING DATE: 1993-01-15
PRIOR PRIOR FILING DATE: 1993-11-17
PRIOR PRILING DATE: 1993-11-17
PRIOR PILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-03
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: CDS

COCATION: (213)..(1325)

OTHER INFORMATION: Description of Artificial Sequence: cDNA insert

OTHER INFORMATION: DampdaTNF-BP15 and pTNF-BP15 vectors
US-09-898-234-11
                                                                                                                                            1321 CTTTGCGGCCCCGCCGCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368
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Best Local Similarity
Matches 1122; Conserv
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APPLICANT: Himmler, Adolph
APPLICANT: Maruer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
APPLICANT: Stratowa, Christian
APPLICANT: Stratowa, Thistian
APPLICANT: Tree of INVENTION: Them
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CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1995-0-01
PRIOR PILING DATE: 1995-0-01
PRIOR PILING DATE: 1995-0-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1900-04-20
PRIOR FILING DATE: 1900-04-20
NUMBER OF SEO ID NOS: 87
SEO ID NO 11
LENGHH: 1334
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Best Local Similarity
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LOCATION: (213)..(1325)
OTHER INFORMATION: Description of Artificial Sequence: C
OTHER INFORMATION: LambdaTNF-BP15 and pTNF-BP15 vectors
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FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 2001-08-17
PRIOR PELLING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/38,676
PRIOR FILING DATE: 1995-02-01
PRIOR PELLING DATE: 1995-02-01
PRIOR PELLING DATE: 1995-01-02
PRIOR PELLING DATE: 1992-01-02
PRIOR PELLING DATE: 1992-01-02
PRIOR PELLING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1900-04-20
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFRENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT APPLICATION NUMBER: US/09/356
PRIOR FILING DATE: 1200-02-23
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1993-11-1430
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEO ID NOS: 97
CURRENT APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEO ID NOS: 97
CHANCE PRIOR PRIOR PRIOR DATE: 1990-04-20
NUMBER OF SEO ID NOS: 97
CHANCE PRIOR PRI
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                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
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                                                                                                                         Sequence 21, Application US/09899429A
Patent No. US20020169118A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (213)...(1325)
US-09-899-429A-21
                                                                                                                                                       GENERAL INFORMATION:
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Search completed: June 9, 2003, 01:17:52 Job time: 214 secs

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Sequence 3, Appli
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CORRESPONDENCE ADDRESS:
ADDRESSEE: 1514 Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
STREET: 0.5.A.
ZIP: 92008
                                                                                                                                                                           US-08-050-319B-53
US-08-04-166-1
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US-08-050-319B-51
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US-08-465-982-49
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          US-08-050-319B-47
US-08-65-982-47
US-08-804-166-7
US-08-910-991-7
US-08-910-991-5
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US-08-928-069-11
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MEDIUM TYPE: 3.5 inch disk, 1.44 Mb COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows NT SOFTWARE: Microsoft Word 97 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A FILING DATE: June 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INN: 514
ATTORNEY AGENT INN: 514
NAME: Laurel Spear Bernstein
REGISTATION NUMBER: 37,280
REFERENCE/COCKET NUMBER: RTS-0004
TELECOMMUNICATION INFORMATION:
TELEFRAX: (760) 931-9200
TELEFRAX: (760) 603-3820
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09106038A Patent No. 6007995 GENERAL INFORMATION:
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 June 9, 2003, 01:14:14; Search time 81 Seconds (without alignments) 1722.690 Million cell updates/sec
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Maximum Match 100%
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Fgapop 6.0 , Fgapext
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                                                                                                                                                             LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla
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Fatent No. 6329148
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TILLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT FILLNG DATE: 2000-02-15
NUMBER OF SOC ID NOS: 4
SOCTWARR: FastSRQ for Windows Version 3.0
SEQ ID NO 3.
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LOCATION: (25)
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                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                           3.09e-229
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                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1456 TACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGGGGGCGCGGGCCTG
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APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WARPOLOWER, Cord
APPLICANT: PRAKEBOLOWER, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR INFURENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY disk
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION DATE: 1107268
FILING APPLICATION DATE: I. 107268
FILING DATE: 12-OCT-1993
ATONINEY/AGENT INPOMBER: II. 107268
FILING DATE: 12-OCT-1993
ATONINEY/AGENT INPOMBER: II. NAME: BROWDY, ROGEL I.
NAME: REGISTRATION NUMBER: 25,618
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Mismatches:
Indels:
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
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Matches:
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TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                               Sequence 1, Application US/08321668
Patent No. 5665859
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
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STRANDEDNESS: single
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ed. No.: 2175 2175 2176 2187.00 Matches: 455 rcent Similarity: 100.00\$ Conservative: 0 ery Match: 100.00\$ Mismatches: 0 ery Match: 1 Gaps: 0 -09-899-422A-2 (1-455) x US-08-837-941-1 (1-2175) 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuLe	Db 256 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGGTGGTGCTCTGGAGCTGTTGGTG 315 Qy 21 GlylleTyrProSerGlyValileGlyLeuValProHisLeuGlyAspArgGluLysArg 40	Db 376 GAIAGIGHIGHTHININININININININININININININININININI	496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	Oy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140	Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180	Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuValIlePhephe 220 Db	Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260 Db	Qy 281 ProthrteudlyPheserProValProSerSerThrPheThrSerSerThrTyrThr 300

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                                                           1216 GCTGACCCCATCCTTGCGACAGCCCTCGACCCCATCCCCAACCCCTTCAGAAG
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 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
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                                                                                              ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly
                                                                                                        AlaaspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
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APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF INFURION: THE RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STARET: D.C.
COUNTRY: USA
ZIP: 20004
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08054970
Patent No. 6395267
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NAME: TOWNSEND, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/POCKET NUMBER: WALLA
TELECOMMUNICATION INFORMATION:
TELEFRONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
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Mismatches:
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Matches:
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100.00%
                                                                         ) NAME_KEY: mat_peptide
; LOCATION: 319..1620
US-08-126-016-1
                                          NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
                     MOLECULE TYPE: CDNA
           linear
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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Fatent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.JC. Turner, F.M Brennan
TITLE OF INVENTION: Modified human Thralpha (Tumor
TITLE OF INVENTION: Modified human Thralpha 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-May-1993
CLASSIFICATION: 435
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NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33, 208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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Matches:
Conservative:
Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
                                                                                                                                                          NAME/KEY: CDS
LOCATION: 256.1620
                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity:
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                                                                                                                        ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly
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                                                                                                                                                                                                                     TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr
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APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
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APPLICATION NUMBER: US/08/050,319
FILING DATE: 10.4May-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                    Indels:
                                                                                                                                                                    8.66e-229
2482.00
99.78%
99.78%
                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
                                                                                                                       155..1519
                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                          NAME/KEY: CDS
                                                                                                                                 US-08-050-319B-24
                                                                                                                                                         Alignment Scores:
                                                                                                                        LOCATION:
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                                                                                      TrpGluaspSeralaHisLysProGloSerLeuaspThraspAspProAlaThrLeuTyr
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                                                                          261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                                                                                                         ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr
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Patent No. 592548
GENERAL INFORMATION:
APPLICANT: Beatler, Bruce A.
APPLICANT: Bazzoni, Flavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON
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Matches:
Conservative:
Mismatches:
Indels:
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  33,208
SR: 5150-0030
REGISTRATION NUMBER: 33,208
REFFRENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                              8.66e-229
2482.00
99.78%
99.78%
                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                      NAME/KEY: CDS
LOCATION: 155.1519
US-08-465-982-24
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Best Local Similarity:
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                                   756 CTAGGICTTTGCCTTCTATCCTTTATCTTCAGGTTTAATGTGCCGATATCCCCGGTGG
                                                                                                                                                                                                                         298 ThrTyrThrProGlyAspCysPro-----AsnPheAlaAlaProArgArgGluVal
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                                                                                                260 GluGlyThrThrLysProLeu----AlaProAsnProSerPheSerProThrPro
                                                                                                                                                            278 GlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSerSer
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APPLICANT: Taylor, J. Michael
APPLICANT: Taylor, J. Macus
APPLICANT: Refirli, Jr., Marcus
APPLICANT: Refirli, Jr., Marcus
APPLICANT: Mwangi, Simon
TITLE OF INVENTION: BOVINE THOR NECROSIS FACTOR RECEPTOR-1
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT FILING DATE: 2000-02-25
PRIOR FILING DATE: 1999-02-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2440
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Patent No. 6406907
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US-09-513-007-1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                  UTSD: 335--1
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY AGENT INFORMATION:
                                           NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERCE/DOKET UNBER: UTSD:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 418-3000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENTH: 1956 base pairs
                                                                                                                                                                                                                                                                                1.8e-136
1521.00
75.61%
65.19%
61.16%
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-762-308-10
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Best Local Similarity:
Query Natch:
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318 TyrGlnGlyAlaAspProlleLeu	336 AsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSerLeuAspThrAsp 		375 ValargargieuGlyLeuSeraspHisGluileaspargLeuGluLeuGlnasnGlyarg 1 1 1 1 1 1 1 1 1	395 CysleubrgGlublaGlnTyrSerMetLeublaThrTrpArgArgArgThrProArgArg	Oy 415 GlualaThrLeuGluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeu 434	Qy 435 GluaspileGluGluAlaLeuCysGlyProAlaalaLeuProProAlaProSerLeuLeu 454	RESULT 11 US-08-286-740-2 ; Sequence 2, Application US/08286740 ; Patent No. 5551053	OEE	; NUMBER OF SEQUENCES: 4 ; CORRESPONDENCE ADDRESSE: Generatech, Inc. ; STREET: 460 Point San Bruno Blvd	5	ADABLE PE: 5.2 IBM PC SYSTEM:	; SOFTWARE: patin (Genentech); CURENT APPLICATION DATA:; APPLICATION NUMBER: US/08/286,740; FILING DATE: 05-AUG-1994	CLASSIFICATION: 435 PRIOR APPLICATION DATA: FILLING DATE:	; ATTORNEY/AGENT INFORMATION: ; NAME: Lee, Wendy M. ; REGISSTRATION NUMBER: ; REFERENCE/DOCKET NUMBER: 798	; TELECHMUNICATION INFORMATION: ; TELEPHONE: ; TELEFAX: 415/952-9881 ; TELEX: 910/371-7168	; INFORMATION FOR SEQ ID NO: 2; ; SEQUENCE CHARACTERISTICS: ; LENGTH: 6889 bases ;; TYPE: nucleic acid
Alignment Scores: 6.23e-136 Length: 2440 Pred. No.: 1517.00 Matches: 302 Score: 30.23* Conservative: 38 Best Local Similarity: 62.92* Mismatches: 104 Query Match: 4 61.00* Indels: 36 DB: 4 Gaps: 7 US-09-899-422A-2 (1-455) x US-09-513-007-1 (1-2440)	1 MetGlyLeuSerThrValProAspLeuLeuDr 	Oy 21 GlylleTyrProSerGlyValileGlyLeuValProHisLeuGlyAspArgGluLysArg 40 :::	<pre>Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60 ::: </pre>	Oy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80	Oy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100	Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120	Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140 	Oy 141 PhedlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160	Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180 ::: ::: :::	OY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200	Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePhe 220	Oy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys 240 ·	Oy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260	Oy 261 GlyThrThrThrLysProLeualaProAsnProSerPheSerProThrProGlyPheThr 280	Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300 [11	Oy 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPro 317

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2490 GATACCCTTATGATTTCCCGGACCCCT-GAGGTCACGTGCTGGTGGACGTGACCT 2548
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                    296 SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArg---GluVal 314
                                                    2352 AAATCTTGTGACACCTCCCCCATGCCCACGTGCCCAGAGCCCAAATCTTGTGACACA
                                                                                                                                                                               315 AlaProPro-TyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIl
                                                                                                                                                                                                                                  -----LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnVal----
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                                                                                                                                                                                                                                                                                                                                                                       384 ulleAspArgLeuGluLeuGlnAsnGlyArgCysLeu---ArgGluAlaGlnTyrSerMe
                                                                                                                                                           334 eProAsnProLeuGlnLysTrpGluAsp-----SerAlaHisLysProGlnSer--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9509576
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                        2412 CCTCCCCATGCCCACGGTGCC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COTTAME: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2639 CACGITCCGIGIGGTCACCGTCCTCACCG 2667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798PCT
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APPLICATION NUMBER: 08/286740
FILLING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee, Wendy M. REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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PCT-US95-09576-2
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Matches:
Conservative:
Mismatches:
Indels:
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1223.50
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59.63%
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Query Match:
STRANDEDNESS:
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                                US-08-286-740-2
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Oy 315 Alabropro-TyrGinGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProll 334	Qy 351 ****LeunspThrAspAspProAlaThrLeuTyrAlaValGluAsnVal 366	OY 367ProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspH1sGl 384	Qy 384 ulleaspargLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGlnTyrSerMe 403	Qy 403 tLeu-alaThrTrpArgArgThrPro 412 1	RESULT 13 US-08-627-151A-6 ; Sequence 6, Application US/08627151A ; Patent No. 5866341	GENERAL INFORMATION: APPLICANT: BECHERER, Kathleen APPLICANT: BECHERER, Kathleen APPLICANT: BROWN, Steven	TVENTION: CONTROL SCI	; ADDRESSEE: Gen-Probe Incorporated ; STREET: 10210 Genetic Center Drive ; CITY: San Diego ; STATE: CA	; COUNTRY: USA ; ZIP: 921D: 921D: ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette	#852	; APPLICATION NUMBER: US/08/627,151A ; FILING DATE: 03-APR-1996 ; CLASS/FICATION: 435 ; PRIOR APPLICATION DATA:	; APPLICATION NUMBER: ; FILING DATE: ; ATTORNEY/AGENT INFORMATION: ; NAME: Fisher Carlos A	RECISTRATION NUMBER: 36,510 REFERENCE/TOCKET UNMBER: CBI016 TELECOMUNICATION INFORMATION: TELEPHONE: 619-410-8926	; TELEFAX: 619-410-8928 ; TELEX: ; INFORMATION FOR SEQ ID NO: 6: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 6896 base pairs ; TYPE: nucleic acid ; STRANDNESS: single ; TOPOLOGY: linear	US-08-627-151A-6 Alignment Scores: 5.62e-104 Length: 6896 Score: 1192.00 Matches: 211
Pred. No.: 5.27e-107 Length: 6889 Score: 1223.50 Matches: 257 Percent Similarity: 64.04% Conservative: 19 Best Local Similarity: 59.63% Mismatches: 61 Query Match: 49.20% Indeals: 95 DB: 5 Gaps: 11 US-09-809-422A-2 (1-455) x PCT-US95-09576-2 (1-6889)	1 MetGlyLeuSerThrValProAspLeuLeuLeuLeuProLeuValLeuLeuGluLeuTeuVal	DD 1805 AIGGGCCICICCACCGIGCCIGCTGCTGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTG	41 AspservalcysprodinglyvsTyrileHisProdinAsnasnserileCysCysThr 	rAsp - - GGAC	Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100 11 1 1 1 1 1 1 1 1 1	Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120	Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140 	<pre>Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 </pre>	Oy 161 LysGlnAsnThrValCysThrCysHisalaGlyPhePheLeuArgGluAsnGluCysVal 180 (Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln11eGlu 200	Qy201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe220	Qy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys 240	Oy 241 SerLysLeuTyrSerlleValCysGlyLysSerThrProGluLysGluGlyGluLeu 259	Qy 260 GludlyThrThrThrLysProLeuAlaProAsnProSerPheSerPro 275 ::	Qy 276 ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer 295	Qy 296 SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArgGluVal 314

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.W Brennan
ITILE OF INVENTION: Modified human INFalpha (Tumor
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Modified human TNFalpha) Receptor
OUNDERSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STREET: California
COUNTRY: USA
LIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
Conservative:
Mismatches:
Indels:
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                                  Gaps:
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47.93%
Percent Similarity:
Best Local Similarity:
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Mismatches:
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Matches:
                 FILING L...
ATTORNEY FAGENT INFORMATION.
NAME: RODDINS, ROBERE 33,208
REGISTRATION NUMBER: 33,208
REFERENCE/CDCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE GOO base pairs
LENGTH: 600 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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  APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNAY AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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Best Local Similarity:
Query Match:
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US-08-050-319B-47
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21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
                        Sequence 47, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.F.Eldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.W Brennan
TITLE OF INVENTION: Modified human ThFalpha (Tumor
TITLE OF SEQUENCES: 57
CORRESPONENCE ADDRESS:
ADDRESSEE: Reed & Robbins
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGRAL OF DEASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         E: Reed & Robbins 635 Bryant Street
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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LOCATION: 1..597
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MOLECULE TYPE:
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US-08-465-982-47
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RESULT 15
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                                                                                                                                            241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACCACCTCAGACTGCCTC
                                                        121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH1sTyrTrpSerGluAsnLeu
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2487 1 MGLSTVPDLILPLVLLELLV......DIEBALCGPAALPPAPSLLR 455 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues 0.5 7.0 7.0 BLOSUM62
Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext Delop 6.0, Delext (US-09-899-422A-2 Title: Perfect score: Scoring table: Sequence: Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	2487		2111	6	HUMTNFRB	M58286 Homo sapien
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30 C	2487	100.0	2161	ه م	AR096330	AR096330 Sequence
10	2487		2175	• •	A43873	A43873 Segmence 1
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4.	2487		2176	w c	A19907	A19907 Synthetic n
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17.	2471	000	2109	0	AK056611	11 Homo as
18	2460		2061		A20255	
19	2444	98.	2050		HUMTNFRP	M60275 Human tumor
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25.	1563.5	. 6	2130	4 W	AE 343370 AXA01925	AYANTOS Semiende
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28	1560.5	62.	2115	_	AF329977	Rattus n
29	1559.5		2115	7	AF329978	Rattus
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36	1521	61.2	2086	101	BC004599	BC004599 Mus muscu
37	1521	61.	2154	7	MUSTINEX	L26349 Mus musculu
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39	1517	61.	2440	-	BTU90937	U90937 Bos taurus
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Homo sapiens
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ACCESSION
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synthetic construct
artificial sequences.
1 (bases 1 to 1368)
Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.
Pur-receptor, TNF-blidding protein and DNA coding therefor Patent: EP 0393438-A 48 24-CCT-1990;
BOBHRINGER INGELHEIM INTERNATIONAL G.M.B.H
       DNA linear From patent EP0393438.
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Synthetic DNA for TNF-receptor f
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelee
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelee
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 2087)
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., W.
Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. an
Goeddel, D.V.
Molecular cloning and expression of a receptor for human to
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by T.Schall, 26-WAR-1990.
Location/Qualifiers
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182. .1549
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Brockhaus, M., Demblo, Z., Gentz, R., Lesslauer, W., Loetscher, H. & Schlaeger, E.J.
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TWF-binding proteins
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F. HOFFMANN-LA ROCHE AG
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	Db 1087 CCGGGGACTGTCCCAACTT Qy 321 AlaaspProlleLeualaTh	Db 1207 TGGGAGGACACCGCCCACAA Qy 361 AlaValValGluAsnValPrv 	Qy 381 SeraspHisGluIleAspAr 	Oy 401 TyrSerMetLeualaThrTr	1447		RESULT 5 AX409713 LOCUS AX409713 DEFINITION Sequence 2360 from Pat.	z ĉ	OKGANISM HOMO SAPIENS ENKATYOLA; Metazoa; Ch Mammalia; Eutheria; Pr REFERENCE 1	י אַ אַ	FEATURES LOCATION/Qual source 12111 /Organism="Ho /db_xref="tax	r 445	Alignment Scores: 2.89e-154 Srod: No.: 2487.00 Percent Similarity: 100.009	uery Match:	US-US-899-42ZA-2 (1-455) X AX4U9/I Qy 1 MetGlyLeuSerThrValPr 	
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Qy 3	381 Serasphis 	GlulleAspArgLe	euGlubeuGlnAsnGl 	SeraspHisGlulleaspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlagln 	1n 400 AA 1386
Qy 4 Db 13	401 TyrSerMet 	LeualathrTrpAi 	rgArgArgThrProAr 	TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 	eu 420 1 TG 1446
Qy 4 Db 14	421 LeuGlyArg 	ValleuArgAspMe 	etaspleuleuglyCy 	LeuGlyargValLeuargAspMetAspLeuLeuGlyCysLeuGluaspIleGluGluali 	la 440
Qy 4	441 LeuCysGly 	ProAlaAlaLeuP)	LeuCysGlyproAlaAlaLeuProProAlaProSerLeuLeuArg	uLeuArg 455 TCTCAGA 1551	
RESULT 5 AX409713 LCCUS DECINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AX409713 Sequence 2360 from AX409713 AX409713.1 GI:214, human. Homo sapiens Eukaryota; Metazoa		111 bp DNA WO0229103.	linear PAT 14.	-JUN-2002
REFERENCE AUTHORS TITLE JOURNAL FEATURES	Manmalia; E Alvares,C., Gene expres Patent: WO GENE LOGIC LC	curneria; Frime Horne, D., Per Saion profiles 0229103-A 236 1010 (US) cation/Qualif. 2111 2111 Prefame From Dryanism Homo	Mammalia; Eurheria; Frimates; Catarinii; in Alvares, C., Horne, D., Peres-da-Silva, S. and Gene expression profiles in liver cancer Patent: Wo 0229103-A 2360 11-APR-2002; GENE LOGIC INC (US) Location/Qualifiers 1. 2111 Corganism="Homo Sapiens" Ab Xref="taxon:9606"	dominidae; j Vockley,	
BASE COUNT ORIGIN	445 a	note="EMBL/Gen1 629 c 58 [°]	Bank Accession N 7 g 450 t	No. M58286"	
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	Scores: milarity: Similarity: h:	2.89e-154 2487.00 100.008 100.008	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2111 455 0 0 0 0	
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1 (bases I to 2112)

1 (bases I to 2112)

Pfizenmaler, A., Maurer-Fogy, I., Kronke, M., Scheurich, P., Pfizenmaler, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C. and Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein

DNA Cell Biol. 9 (10), 705-715 (1990)
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Pred. No.: Score: Score: Score: Score: 2.89e-154 Matches: 455 Percent Similarity: 100.003 Mismatches: 0 Best Local Similarity: 100.003 Mismatches: 0 Indels: 0 Indel	LIVSARG SAAGAGA 	61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	lAsp - - - - - - - - - - - -	Oy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160	Qy 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200 Db 747 TCCTGTAGTAACTGTAAGAAAAGCCTGGACTGCACCAGATTGAG 806 Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	241 SerLysLeutyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2161)
Nophary: Kemper,O. Brakebusch,C., Englemann,H., Zwang,R.,
Aderka,D., Holtmann,H. and Wallach,D.
Solubbe forms of tumor necrosis factor receptors (TNF-Rs). The of or the type I TNF-R, cloned using amino acid sequence data of soluble form, encodes both the cell surface and a soluble form of
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256. 2161
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Unclassified. REFERENCE 1 (bases 1 to 2175) AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D. TITLE Expression of the recombinant tumor necrosis factor binding protein 1 (TBP-I) JOURNAL Patent: US 5811261-A 1 22-SEP-1998; FEATURES 1. 22755 SOURCE /Organism="unknown" BASE COUNT 474 a 641 c 604 g 456 t	Alignment Scores: 2.99e-154 Length: 2175 Pred. No.: 2487.00 Matches: 455 Score: 2487.00 Matches: 455 Percent Similarity: 100.00% Mismatche: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 6 Gaps: 0	1017-1017-1017-1017-1017-1017-1017-1017	Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnasnSerIleCysCysThr 60	91 CysArgGluGysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100	Oy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140	Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180	Oy 201 AsnValLysGlyThrGluAapSerGlyThrThrValLeuLeuDroLeuValllePhePhe 220
141 PheclnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	201 856 221 916 241	Db 976 TCCAAGCTCTACTCCATTGTTGTGGGAAATCGACGTGAAAAAGAGGGGGGGG	301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 1156 CCCGGTGACTGTCCCACCTTTGCGGCTCCCCGCAGGGGGGGG	DD 1210 GCTGACCCCATCCTTGCGACAGCCCTCGGACCCCGACCCCCATCCCCAACCCCTTCAGAAG 1275 QY 341 TrpGluAspSerAlaHislysProGluSerLeuAspThrAspAspProAlaThrLeuTyr 360 1276 TGGGAGGACAGCCCCACAAGCCACAGCCCTAGACCTGATGACCCCGCGCACGCTGTAC 1335 QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380 DD 1336 GCCTGGAGGAACGTCCCCCTTGCACAAATCTCCCCCCCCC	381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 111111111111111111111111111111111111	1 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440	RESULT 12 AR041076 LOCUS LOCUS DEFINITION SEQUENCE 1 from patent US 5811261. ACCESSION AR041076. VERSION AR041076.1 GI:5961572 KEYWORDS SOURCE ORNOWN.

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1 (Lobases 1 to 1076)

NIH-MCC.http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://mage.llni.gov

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source

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Score

Result

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BQ723672
AGENCOURT_8489850 Lupski_dorsal_root_ganglion Homo saplens cDNA clone IMAGE:6184295 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov
Email: capabs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://magge.llnl.gov
Plate: LLAM13573 row: d column: 24
High quality sequence stop: 607.
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NIH-WGC http://mgc.not.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="pH108"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1: Site_2: Sall; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
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/organism-"Homo sapiens"
/db_xref-taxon:9606"
/clone="IMAGE:6184.295"
/clone_lib="Lupski_dorsal_root_ganglion"
                                          204 t
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283 c
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                                                                                               /note=*Organ: pooled colon, kidney, stomach; Vector:
pCNV-SPORT6; Site_1: NotI: Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full:length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library.*

6 a 356 c 303 g 205 t 6 others
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/clone="IMAGE:5758757"
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/lab_host="DH10B"
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pWE18SFL3"
301 c 249 g 166 t 6 other:
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/db_xref="taxon:9606"
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1532-3 Yana, Kisarazu, Ch
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
E | Deass 1 to 741)
Es | NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emal: cgapbs-rémail.nih.gov
Tissue Procurement: EufD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MG.E. Consortium/LLNL at:
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
High quality sequence stop: 740.
Location/Qualifiers
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/organism="Homo saplens"
/organism="Homo saplens"
/organism="Homo saplens"
/clone=lib="NIH_MGC_87"
/clone=lib="NIH_MGC_87"
/tlab_host="DH10B (phage=resistant)"
/note="Organ: breast; Vector: pcMV-SpORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Notespee insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                           603390284F1 NIH_MGC_87 Homo saplens cDNA clone IMAGE:5399108 5', BI860918
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Indels
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/cell_type="teratocarcinoma"
/cell_type="teratocarcinoma"
/cell_type="teratocarcinoma"
/note="vector: pkEl8SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
a 199 c 201 g 179 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3966
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
Hri human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                            62 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGGTGGTG
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                                                                                                                                                                                                                                                                                        ch 49.9%; Score 682.4; DB 9; 11 Similarity 99.1%; Pred. No. 6.1e-158; 694; Conservative 0; Mismatches 5;
                                                                                                                      Location/Qualifiers
                                                                                                          Helix Research Institute
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 761)

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                                                                                                                                                                                                                                                                                                                                                                                                                    .085 TGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCCTAGGGCTGAGGCGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGATTCGTGCGGCGCGCTGAGGGCTGAGGGCTGAGGGCGCGTGGGGCTGAGGGCGCGTGGGGCTGAGGGCG
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                                                                                                                                                                                                                                                                GTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGTGGCACCACCCTATCAGGGGGGCTG
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                           Indels
 Score 689; DB 9; I
Pred. No. 1.5e-159;
0; Mismatches 3;
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
  50.4%;
                           Conservative
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HRI human
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/lab_host="DH10B"
/lab_host="DH10B"
/notc="Organ: brain; Vector: pCMVSPORT 6; ist strand cDNA
was primed with a NotI-ollgo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filangelifetech.com URL:
http://tullength.invitrogen.com"
3 others
                                                       AL529836 ALI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD005YP05 5
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                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
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                                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                               /organism-"Homo sapiens"
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                                                                                                                 AL529836.1 GI:12793329
                                                                                       mRNA sequence.
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1 (Dases 1 to 1070)

RS NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Techno
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AGENCOURT_6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723557
5', mRNA sequence.
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Pred. No. 2.8e-157;
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                                               : www.genoscope.cns.fr
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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Pred. No. 6.9e-157;
4; Mismatches 8;
                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
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Best Local Similarity 97.9%;
Matches 704; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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BG180101 974 bp mRNA linear EST 06-FEB-2001 602329676F1 NIH_MGC_91 Homo sapiens CDNA clone INAGE:4431019 5', mRNA sequence.
BG180101 GI:12686804
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National Institutes of Health, Mammalian Gene Collection (MGC)

Onpublished (1999)

Londatt: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://langat.llnl.gov

Plate: LLAM10185 row: g column: 20

High quality sequence stop: 657.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 974)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (basas 1 to 669)

RS Kim,N.S., Eahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,N.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

MILM,Y.S.

ZIC Frontier Korean EST Project 2001

Unpublished (2002)

Coltact: Kim YS

Genome Research Center

Korea Research Center

Korea Research Institute of Bioscience & Biotechnology

Genome Research Lostitute of Bioscience & Biotechnology

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100.0%; Pred. No. 1.2e-154;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Ascites"
/coll_type="Scattering floating"
/cell_line="sNU-620"
/lab_host="ToplOF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-5-c12"
/clone=11b="S6SNU620"
/sex="F"
                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BM742386
BM742388.1 GI:19063703
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Best Local Similarity
Matches 669; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
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BM742388
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AUTHORS
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/note-organ: Lung, Vector: pT737-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I: Not_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into PT737-Pac vector. The oilgonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838 ACCCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTAT 897
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iow
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iow
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iow
CON DISTRIBUTION: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LiNi at: http://image.lini.gov
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                    NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 TTTGGTCTTTGCCTTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGG
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IMAGE:5862208 3', mRNA sequence.
BM989994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_DIO"
/tlssue_type="Lung Focal Fibrosis"
/dev stage="Adult"
/lab_host="DHIOB (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%; Score 667.8; DB 14;
98.0%; Pred. No. 2.4e-154;
Live 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_TISSUE-lung with fibrosis
TAG_SEQ-ATACGCGGTC"
244 c 190 q 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5862208"
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                                                                                  BM989994,1 GI:19709383
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                                                                                                                           human.
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/db_xref="taxon:9606"
/clone="IMAGE:4431019"
/clone=lib=NHH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tab_host="bullob (phage=resistant)"
/note="Organ: prostate; vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

>note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                           Length 974;
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Pred. No. 1.6e-154;
0; Mismatches 34; Indels
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994 bp mRNA linear EST 05-MAR-2002
AGNCOURT_6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041
BM800044
                                                                                                                                654 ITTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACG 713
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 994)
                                                                                                                                                                                                             241 CTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGGGGCACCACATA
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                                                                                                                                                                                                                                                                                                                              CTTCACCCCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCAC
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National Institutes of Health, Mammallan Gene Collection (MCC)
Unpublished (1999)
                                                                                                    Gaps
   a NCI_CGAP Library."
                                                                                                    ä
                                                                                                  Indels
                                                                   Length
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                                                                Score 667; DB 12;
Pred. No. 3.8e-154;
0; Mismatches 10;
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                                                              tch 48.8%;
al Similarity 98.4%;
684; Conservative
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1. I (bases 1 to 718)

1. I (bases 1 to 718)

1. I (bases 1 to 718)

1. Indicination (mgc. nci.nih.gov/.

1. Mational Institutes of Health, Mammalian Gene Collection (MgC)

1. Indublished (1999)

1. Contact: Robert Strausberg, Ph.D.

2. Email: cgapbs-rémail.nih.gov

1. Tissue Procurement: Life Technologies, Inc.

2. CDNA Library Preparation: Life Technologies, Inc.

2. CDNA Library Preparation: Life Technologies, Inc.

3. CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Localian/Quality sequence stop: 679.

1. Localian/Qualifiers

1. Localian/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        718 bp mRNA linear EST 01-MAY-2001 602626965F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751536 5', mRNA sequence.
BG880679
BG80679.1 GI:13912076
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Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCTTTGCGGCCCCGCCCTCCCGCC 1346
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TITLE
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1073

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FEATURES

1013

360

120

833

893 240 953 300

773

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Query.Match
Best Local Similarity 99.8'
Matches 639; Conservative
                                                                                                                                                                     human.
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AL522989
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                                                                                                               /organism="Homo sapiens"
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Average insert size 2.1 kb. " 3 others
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                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MNA Sequencing by: Agenceurt Bioscience Corporation
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                               Length 994;
                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                               Score 647.2; DB 14;
Pred. No. 3.2e-149;
0; Mismatches 31; 1
 Ph.D.
                                                                                               High quality sequence stop: 654.
Contact: Robert Strausberg, Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.7%;
Matches 713; Conservative
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/u.e., /
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8371 Email: filang@lifetech.com URL:
http://fullength.invitrogen.com"
10thers
                                                                                                                                                                                                                                                         AL522989 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB009YP14 5
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658 TITIGGTCTTTGCCTTTTATCCCTCTTCATT---GGTTTAATGTATCGCTACC---AA 711
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          826 ITTGGGCTTGCCCTTTATCCCTCCCCTCCATTGGGTTTAAATGGATCGCTACCCCACG
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualiflers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length Chon 11braries and normalization
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Score 638.4; DB 9 99.8%; Pred. No. 4.6e-147 Live 0; Mismatches 1
                                                                                    prime, mRNA sequence.
AL522989
AL522989.1 GI:12786482
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438 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 497

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	c O		421 TTCCAGTGCTTCAATTGCAGCGTCTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480	618 TICCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACGTGCACCTCTCCTGCCAGGAG 677	481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC	678 AAACAGAACACCGTGCCATGCAGTTTTCTTTCTAAGAAAACGAGTGTGTC 737	541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600	738 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTCTGCCCAGATTGAG 797	601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGT 640	798 AATGITAAGGGCACIGAGGACTCAGGCACCACAGIGCTGT 837
o d	3 8	q	δŏ	ą	Qy	q	ò	qa	ò	ą

Search completed: June 9, 2003, 00:13:31 Job time: 1870 secs SUMMARIES

OM protein - nucleic search, using frame_plus_p2n model

June

Run on:

8, 2003, 23:42:19; Search time 299 Seconds (without alignments) 3426.954 Million cell updates/sec

US-09-899-422A-2 Title: Perfect score: Sequence:

2487 1 MGLSTVPDLLLIPLVLLELLV......DIEEALCGPAALPPAPSLLR

455

BLOSUM62 Scoring table:

2.007 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2185239 seqs, 1125999159 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AAQ49932 standard; cDNA to mRNA; 1368

BP.

AAQ49932;

29-APR-1994 (first entry)

Lambda-derived INF-R CDNA.

Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF: IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;

autoimmune dysfunction; ss.

Homo sapiens

N

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                                             LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
                                                                                        AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePhe
                                                                                                                                                                                                                                                                                                                                                                                                         121 GATAGTGTGTGTCCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC
                                                         241 TGCAGGGGGTGTGAGGGCTCCTTCACCGCTTCAGAAACCACCTCAGACACACTC
                                                                                                                                     SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp
                                                                                                                                                                                                                                       ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH1sTyrTrpSerGluAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr
                                                                                                                                                  CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                             PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
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                                                                                                                                                                                                                                                                        LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its blological activity. These fusion proteins may be used in therapy, disponsis and assays for conditions may be used in particularly in conditions in which both TNF and iL-1 particularly in conditions in which both TNF and iL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, cerebral malaria, allograft and xenograft fibrosis and salicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                               necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuUeuVal
                                                                                                                                                                                                                                                                                                                                                                                   in the
                                                                                                                                                                                                                                                                                           New fusion protein tumour necrosis factor and human interleukin-1
                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAQ49931-32 encode human tumour necrosis receptor (TNF*R) and the sequences in AAQ49933-34 encode human interleukin-1 receptor (IL-1R). These sequences were used in production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                       useful in therapy, diagnosis and assays of e.g. arthritis, diabetes, cerebral malaria, sepsis, etc
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                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 57-59; 85pp; English.
                   Location/Qualifiers
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1..1366 a /
*tag b /
*tag b /
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IL-1R-11nker-TNF-R-11nker-TNF-R
TNF-R-11nker-TNF-R
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Lambda-gt10-7-ctnfbp
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Best Local Similarity:
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Pred. No.:
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rheumatoid
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TNFR1; tumour necrosis factor receptor; polymorphism; human; tumour; cancer; apoptosis; bacterial infection; ds.
                             Location/Qualifiers
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                                                       AAA95105 standard; DNA; 1368 BP
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1058..1368
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                                                                                 Human TNFR1 coding sequence
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/product= '
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/*tag= b
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626..739
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                                               RESULT 2
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The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNRR1) gene. The present sequence is the coding sequence of the TNRR1 gene. The sequence of the whole gene is given in AAA95102, AAA95103 and AAA95104. The polymorphisms were identified by amplifying and sequencing regions of the gene. Twelve polymorphis loci were discovered. Of these twelve polymorphisms, four can cause a change in the TNRR1 protein. The TNRR1 polymorphisms may be identifying trageting the biological function of TNRR1 as well as for identifying druge targeting the protein for treatment of disorders related to its abnormal expression or function such as tumours, apoptosis related disorders and bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the blological function of TNFR1 and identifying drugs targeting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
                                                                                                                                                                                                                                            Chew A;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           protein for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fig 4; 79pp; English.
                                                                                           GENAISSANCE PHARM INC.
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2487.00
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100.008
                                                99US-0121314.
23-FEB-2000; 2000WO-US04606.
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                                                                                                                     NANDABALAN K.
SCHULZ V P.
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P-PSDB; AAB23446.
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Best Local Similarity:
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                                                23-FEB-1999;
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The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gill using a probe (AAQ20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also AAQ20974.
                                                                                                                                                   /note- homologous to probe AAQ20974"
242..751
/*tag- e
/note- "encodes the extracellular domain of human
                                     9
                                                                                                                                                                                                                                                                                                                                    New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis
                                   factor alpha; autoimmune diseases; cachectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T; 0 other;
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Matches:
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Indels:
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                                                                            Location/Qualifiers
155..1522
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                  TNF-alpha binding protein gene
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  11-MAY-1992 (first entry)
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155..274
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                                           extracellular domain.
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P-PSDB; AAR20787.
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                                                            Homo saplens
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                                                                                         AlaaspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
                        PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                                                                                                            AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe
                                                                                                                                                            GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys
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This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA library in gt10 was screened with probe AAQ29236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The inserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha
                       comprises
                                                                                                                                                                   tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection;
malaria; viral meningits; graft versus host disease;
autolimmune disease; rheumatoid arthritis.
                                                      New polypeptide capable of binding human TNF alpha - compri-
first three cysteine-rich subdomains of TNF alpha receptor
treating autoimmune disease, septic shock, HIV etc.
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'codon= Seq"AAG",
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P-PSDB; AAR24000.
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                275 GATAGTGTGTGTCCCCAAGGAAATATATCCACCTCAAAATAATTGGATTTGCTGTACC
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89US-0381080.
89US-0450329.
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                                                                                                                                         55kD receptor was isolated as an ECORI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in prinkr. A derivative of the TNF-alpha receptor was produced by domain. PCR with primers AQQ9237,8 generated a 300pp restriction fragment which was cloned into prinkr, giving prinked by DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.
                                                                                                                                                                 GlylleTyrProSerGlyVallleGlyLeuValProHisLeuGlyAspArgGluLysArg
                                                                                                                                                                                                                                               CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
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                                                                  BP; 429 A; 618 C; 572 G; 443 T; 0 other;
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Matches:
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171..1536
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                          GGAACTACTACTACTCCCCTGGCCCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTCAC
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                 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu
                                                       GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                                                                                                                                                                                                                                                                                                                                                                                     TNF inhibitor; antlinflammatory; Tumour Necrosis Factor; IL-1; inflammatory disease; degenerative disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human 30 kDa TNF inhibitor precursor coding sequence
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18-JUL-1989;
11-DEC-1989;
07-FEB-1990;
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                                                                            which the sequence was obtd, was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                   uur necrosis factor inhibitor - for suppression of TNF-alpha
-beta, useful as therapeutic agent.
                                                                   inhibitor. The clone
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                                                                  sequence encodes the entire 30 kD TNF
                                                                                                                           See also AAQ10878, AAQ10884 and AAQ10907
                                                                                                                                                                                                                                           (1-2088)
                                                 Disclosure; Fig 21; 142pp; English
                                                                                                                                              Sequence 2088 BP; 439 A; 626 C;
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                                                                                                                                                                       2.96e-174
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Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated
                     Hale K
Lce J,
               Squires C, King MW, Hal
Vanderslice RW, Vannice
                                         WPI; 2001-006443/01
P-PSDB; AAB37677.
  AMGEN INC
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The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic for treating inflammatory and degenerative diseases mediated by TNF. I), and present sequence is the coding sequence for the precursor of 30 kDa TNF inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha. Example 6; Fig 21; 82pp; English.

Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

2088 455 0 0 0 Length:
Matches:
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TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCCACGAAGTTGTGCCTACCCCAGATTGAG 768 220 828 240 888 1068 948 1128 1129 GCTGACCCATCCTTGCGACAGCCCTCGGCCCCCATCCCCAACCCCTTCAGAAG 1188 260 291 ProThrLeuglyPheSerProvalProSerSerThrPheThrSerSerSerThrTyrThr 300 1308 380 1488 400 420 440 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 889 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAGAGGGGGAGCTTGAA SerLysLeuTyrSerIlevalCysGlyLysSerThrProGluLysGluGlyGluLeuGlu AlaAspProlleLeualaThralaLeualaSerAspProlleProAspProLeuGlnLys SerAspHisGlulleAspArgleuGluleuGlaAsnGlyArgCysLeuArgGluAlaGla , A 201 692 607 241 301 1069 321 . 1009 381 1309 AAZ09170 ď õ 셤 à 유 ö g à d g δŏ ò g 셤 ò g ð 셤 ò 윱 ò g ó d å 셤

AAZ09170 standard; cDNA; 2111

(first entry) 18-OCT-1999 AAZ09170;

necrosis factor binding protein cDNA. Human tumour

Tumour necrosis factor binding protein; TNF; insoluble protein; agonist; anti-inflammatory; antimalarial; treatment; septic shock; inflammation; autoimmune glomerulonephritis; cerebral malaria; immune response; antagonist; diagnosis; ds. TO NAME OF THE PART OF THE PAR

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           SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp
                                                    PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                                                                                          SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu
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                                AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGCACAGTGGAC
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                                                                                                                                                                                                                                                                      New insoluble proteins, and fragments, that bind to tumor necrosis factor, used to treat e.g. septic shock or cerebral malaria
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89CH-0003319.
90CH-0000746.
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12-SEP-1989;
08-MAR-1990;
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Schlaeger E;
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                                                                                      TNF; tumor necrosis factor binding protein; TNFBP; treatment; insoluble protein; antiinflammatory; immunosuppressive; antibacterial; antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; autoimmune glomerulonephritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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                                                                   Human TNFBP-associated DNA #1
     AAH48859 standard; DNA; 2111
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90CH-0001347.
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Schlaeger E;
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20-APR-1990;
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Pred. No.:
                           AAH48859;
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

3e-174 2487.00 100.008 100.008 100.008

Percent Similarity: Best Local Similarity: Query Match: DB:

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     1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuLeuVal
                                   CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
                                                                            141 PheGinCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                                                                                                 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe
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          The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the
                                                           400
                                                                                                         401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                           SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln
                                                                                                                                                                                                                                                                                                                                                                                Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in granulocytic cells #610.
                                                                                                                                                                                                          Vockley J;
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                                                                                                                                                                                                                                                                                   ABK84039 standard; cDNA; 2111 BP
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control of the tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the subject to apathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; where the level of expression of the gene is indicative of inflammation.

CC (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting GA; MS is useful for contacting an inflammation in a tissue; M4 is useful for modulating GA; MS is useful for screening an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, arbina; creperfusion injury, ARDS, adult respiratory distress syndrome, creperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present consecuted and for a protozoal infection, fungal infection for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal
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Query Match:
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93303-ABN97455 in a cytostatic attivity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic cytostatic activity. The method is useful diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic carcinoma in a patient. The method is useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, of markers that can be used to monitor disease states, disease progression, of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                           Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2360; 298pp; English.
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    AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
                           SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu
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                                                                                ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr
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                      PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                        LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal
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The invention provides antisense compounds targeted to human tumour necrosis factor receptor type 1 (TNRT1) RNA. These antisense compounds can be used in a method of inhibiting the expression of INFR1 human cells or tissues. The antisense compounds specifically hybridize with one-or more nucleic acids encoding INFR1 modulating the function of nucleic acid molecules encoding INFR1, ultimately modulating the amount of INFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. The present sequence represents the nucleotide sequence of human INFR1 (GenBank Accn No: X55313).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense inhibition of tumor necrosis factor type 1 expression for diagnosis, treatment and prevention of disease, particularly tumors
                                     is factor receptor type 1; TNFR1; antisense; infection; tumour formation; TNFR1; anticancer; ds.
Human tumour necrosis factor receptor (TNFR1) nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604 G; 456 T; 0 other;
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                               Antisense inhibition of
                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                     Baker BF, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-105333/09.
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Best Local Similarity:
Query Match:
                                       necrosis
                                                       inflammation;
                                                                                              Homo sapiens
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                                                                                                                        SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu
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This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic condination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking triepoxide. This method has cytostatic activity and works by blocking two for TNF-alpha mediated induction of C-TAP2 and c-TAP1. The method of the invention may be used for treating tumours, particularly solid tumours, c. arctinoma, mammary adenocarchoma and non-small cell lung carcinoma also neurological malignancies, non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, my grossis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphold hyperplasis, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. antimetastatic, anti-tumour or anti-angiogenic agents. The potent synergy between the diterpenoids and the death domain ligands allows increased resistant cells. This sequence ropresents the human tumour necrosis factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor cueed in the used method of the invention in combination with diterpenoid triep appearance or combination or and combination of combination or combination and combination or combination and combination or combination and combination or combination and combination with diterpenoid
                                                                                                                                                                             diterpendid triapoxide; oytostatic activity; c-IAPJ; c-IAPJ; c-Cardinoms, mammary adenocarcinoms, non-small cell lung carcinoms, neurological malignancy; lichem planus; non-Bodgkin's lymphoms; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic; non-NF cutaneous T-cell; lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human; gene; receptor; TNF-RI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumour cells
                                                                                                                                                                      receptor 11gand;
                                                                                                                     Human tumour necrosis factor alpha (TNF alpha) receptor DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
                                                                                                                                                                  ds; tumour; death domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha protein"
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256..1623
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99US-149989P.
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                                                                               (first entry)
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P-PSDB; AAU75064.
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20-AUG-1999;
                                                                               23-APR-2002
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2161

Length:

Alignment Scores: Pred. No.:

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Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorabol myristate accetate (PMA).

C depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AAR75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane confiners between human p55 TNF-R and murine epidermal growth factor receptor (BGF-R) that are represented by AAR75007-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions (AAR75056-47). Of the spacer region, the most important residues are can important of these. The shedding of the receptor is independent of the conformation of the protein adversely effect the shedding process. The conformation of the protein adversely effect the shedding process. The from the cell bound TNF-R. Fragments of these inhibitors can be seen in thithier of a protease that is capable of cleaving the soluble TNF-R. ANR75013-4. These protease
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Mismatches:
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            SerLysLeuTyrSerlleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu
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                                                                                                                                                                            AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
                                                                                                                                                                                                                                 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu
                                                                                                                                                                                                                                                                                                                                            Tumour Necrosis Factor; binding proteins; septic shock; autoimmune glomerulonephritis; lymphokine; cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                            Encodes human 55kD TNF-binding protein.
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AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
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                                                                                                                                                                                                                          Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs (see AAR11072.R11081) and oilgonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda gtll. Positive clones were identified and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer lamproved TNF-binding properties.
                                                                                                                                                                  Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody prodn.
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89CH-0003319.
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Schlaeger EJ;
                                                           20-APR-1990;
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08-MAR-1990;
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                                                                SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF; tumour necrosis factor; receptor; disease; autoimmunity; rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                         Modification of the tumour necrosis factor receptor by mutation or deletion modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor.

Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated with TNF activity e.g. autoimmume disease; rheumatoid arthritis; graft rejection; graft vs. host disease or septic shock. They can also be used to treat overdoses of exogenous TNF.
                                                                                                                                                                                                                                                                                                                     Modulating activity of tumour necrosis factor receptor - using peptide(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto-immune disease, septic shock, etc.
                                                                                                                                       necrosis factor receptor
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-899-422A-1

Title:

1 atgggcctctccaccgtgcc......cgcccagtcttctcagatga 1368 Perfect score: Sequence:

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2185239 seqs, 1125999159 residues Searched:

4370478

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDS2/gcddata/geneseq_geneseqn_embl_NAl980_DAT:*
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| SIDS2/gcddata/geneseq_geneseqn_embl_NAl991_DAT:*
| SIDS2/gcddata/geneseq_geneseqn_embl_NAl992_DAT:* N_Geneseq_101002:*

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/SIDS2/gcgdata/geneseq/genesegn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001B.DAT:*

/SIDS2/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Lambda-derived TNF	Human TNFR1 coding	30kD INF inhibitor	Human 30 kDa TNF i	Human tumour necro	Human INFBP-associ	Human cDNA differe	Gene #2360 used to	Human tumour necro
SUMMARIES			ΩI	AAQ49932	AAA95105	AAQ10883	AAC83946	AAZ09170	AAH48859	ABK84039	ABN95862	AAZ48475
			099	14	21	12	22	20	52	24	24	21
			Match Length DB I	1368	1368	2088	2088	2111	2111	2111	2111	2161
	æ	Query	Match	6.66	66.66	66.6	66.66	6.66	66.66	66.66	66.66	6'66
			Score	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4
		Result	NO.	-	7	m	4	S	ø	7	60	σ

Human tumour necro Encodes human 55kD p55 TNF-8 pene. H TNF-alpha binding Encodes TNF-alpha Type I TNF recepto Human Tumour Necro p55 Tumnour necrosi P15 Fumour Necro P55 Tumour necrosi P15 Fumour Necro Rat Tumour Necro CadC-fusion polype CDNA for TBP(20-19 Encodes truncated Human soluble tumo Soluble tumour necro Tumour necrosis in Human 30 kDa TNF i Partial human TNFR CDNA for TBP(20-16 Malfe fusion plasmi TNF-selectokine pr Encodes truncated	Target canine gene Encodes truncated Nucleotide sequenc Truncated SINFR, s Encodes truncated Truncated SINFR, s Truncated SINFR, s
	ABL99490 AAQ24442 AAA19044 AAV19804 AAQ24443 AAV19805 AAV19805
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2161 22111 22111 22052 2062 2117 21170 21130 6089 6089 6089 6089 6089 6089 6089 608	00 4 00 4 00 00 4 00 00 4 00 00 8 00 00 8 00 8
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ALIGNMENTS

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AAQ49932 standard; cDNA to mRNA; 1368 BP
                                                                                                          29-APR-1994 (first entry)
                                                                                                                                              Lambda-derived INF-R cDNA.
                                                                         AAQ49932;
RESULT 1
AAQ49932
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Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF; IL-1; cachexis; cerebral malaris; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allicosis; allicosis; allicosis; inflammation; rejection; graft verses host disease; sepsis; inflammation; allergy;

Location/Qualifiers
1..1366
/*tag= a /*tag= a 1..120
1..120
/*tag= b 1.12.1.1363
/*tag= c autoimmune dysfunction; ss Lambda-gt10-7-ctnfbp. Homo saptens Key

W09319777-A.

sig_peptide mat_peptide 14-0CT-1993

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                                                                AATGITAAGGGCACTGAGGACTCAGGCACACAGTGCTGTTGCCCCTGGTCAIITICIII
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                                                                                                                                                                                                                                                                                                                                      The Inker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeitles by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple solerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    The sequences given in AAQ49931-32 encode human tumour necrosis fireceptor (INF-R) and the sequences in AAQ49933-34 encode human interleukin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                         protein tumour necrosis factor and human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 1368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                     receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1366.4; I
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                   TNF-R-11nker-TNF-R-11nker-IL-1R
IL-1R-11nker-TNF-R-11nker-TNF-R OF
TNF-R-11nker-TNF-R
                                                                                                                                                                                                            Disclosure; Page 57-59; 85pp; English.
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           93WO-US02938
                                     92US-0860710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.9
Matches 1367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune dysfunctions
                                                              (IMMV) IMMUNEX CORP
                                                                                                                  WPI; 1993-336592/42.
                                                                                                                                P-PSDB; AAR42059
                                     30-MAR-1992;
                                                                                                                                                        New fusion
                                                                                        Smith CA;
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 biological function of TNFR1 and identifying drugs targeting the
                                                                                                                                                                                                                                                                  Score 1366.4; DB 21; Length 1368;
Pred. No. 0;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                        Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
              protein for treating disorders
                                          Claim 7; Fig 4; 79pp; English.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 1367; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
                          TNFR1; tumour necrosis factor receptor; polymorphism; human; tumour; cancer; apoptosis; bacterial infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chew A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stephens JC,
                                                                                             Cocation/Qualifiers
1..1368
/*tag= a
                                                                                                                        /*tag= a
/product= "TNFR1"
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replace(224,T)
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Human TNFR1 coding sequence.
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740..768
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SCHULZ V P.
STEPHENS J C.
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                                                                          The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a cDNA library prepol. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted inco expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                                         DB 12; Length 2088;
                              of INF-alpha
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                                                                                                                                                                                            1; Indels
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                               suppression
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99.9%; Score 1366.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches
                                                                                                                                                      Sequence 2088 BP; 439 A; 626 C; 578 G; 445
                                                                                                                                   See also AAQ10878, AAQ10884 and AAQ10907
                             our necrosis factor inhibitor - for -beta, useful as therapeutic agent.
                                                         Disclosure, Fig 21; 142pp; English
  WPI; 1991-073847/11
          P-PSDB; AAR10986
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                             GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGGTTCAGTCCCACTCCAGGCTTCACC
                                                       CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC
                                                                                             CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG
                                                                                                                                                   GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
                                                                                                                                                                      TGGAGGACAGCGCCCACAGAGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTAC
                                                                                                                                                                                                           GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
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171..1536
/*tag= a
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89US-0381080.
89US-0450329.
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The present invention relates to Tumour Necrosis Factor (TNF) inhibitors dee AAB37676 and AAB37685), which have Thr Inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the coding sequence for the precursor of 30 kDa TNF inhibitor. TNF alpha.
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                                 Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated with -
                                                                                                                                                                                           DB 22; Length 2088;
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                                                                                                                                                                        Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
                                                                                                                                                                                                             ;
                                                                                                                                                                                          99.9%; Score 1366.4; llarity 99.9%; Pred. No. 0; Conservative 0; Mismatches
                                                                                82pp; English
      WPI; 2001-006443/01
P-PSDB; AAB37677.
                                                                               Example 6; Fig 21;
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Matches 1367;
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                                                                                                                  GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
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                                          CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC
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                                                                                                                                                                                                                                                                                                                                                   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; IL-1; inflammatory disease; degenerative disease; human;
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Kohno T;
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Vanderslice RW, Vannice J, Ko
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93US-0090366.
89US-0381080.
89US-0450329.
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09-JUL-1993;
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11-DEC-1989;
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GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
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TNF: tumor necrosis factor binding protein; TNFBP; treatment; insoluble protein; antiinflammatory; immunosuppressive; antibacterial; antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; autoimmune glomerulonephritis; ds.
                                                                                         GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG
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             TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
                                      AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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                                            Location/Qualifiers
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31-AUG-1990;
Homo sapiens
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                      Human; 88; granulocytic cell; DNA chip; bacterial infection, viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatorid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                    Human cDNA differentially expressed in granulocytic cells #610.
                                                                                                                                                                                                                                                                                                                                     Vockley J;
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                      В.
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                    ABK84039 standard; cDNA; 2111
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                                                              (first entry)
                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
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                                                             14-AUG-2002
                                         ABK84039;
RESULT 7
ABK84039
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inflammatory disease (e.g. psoriasis, rheumatoid arthritis, gonerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, response in a subject, exposure of a subject to a pathogen or sterile

Claim 1; SEQ ID No 610; 114pp; English.

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parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at format directly from WIPO at
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Pred. No. 0;
0; Mismatches
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Matches 1367; Conserv
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CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCG
                                                GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
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                                                                           TGGGAGGACACCACAAGCCACAGAGCTAGACACTGATGACCCCGGCGACGCTGTAC
                                                                                                                 Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease stidisease progression; drug toxicity; drug efficacy; drug metabolism.
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tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN83503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnossing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, entry coxility, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.WIPO.Int/pub/published_pct_sequences.
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Pred. No. 0;
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The invention provides antisense compounds targeted to human tumour necrosis factor receptor type I (TNFR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNFR1 human cells or tissues. The antisense compounds specifically hybridize with one or more nucleic acids encoding TNFR1 untimately modulating the function of nucleic acid molecules encoding TNFR1 ultimately modulating the amount of TNFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. The present sequence tepresents the nucleotide sequence of human TNFR1 (GenBank Accn No: X55313).
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                1036 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC
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                                                                                                                                                                             This invention relates to a novel method for enhanced killing of tumour cells accomprising contacting a tumour cell with a syncrgistic combination of a death domain receptor ligand and a diterpencial triepoxide. This method has cytostatic activity and works by blocking triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-Mr cutaneous T-cell lymphoma, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. antimetastatic, anti-tumour or anti-angiogenic agents. The potent synergy netween the diterpenoids and the death domain ligands allows increased xilling at equivalent or lower doses, and can sensitiae otherwise resistant cells. This sequence represents the human tumour necrosis factor alpha receptor (TNF-RI) DNA. TNF-RI is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by inducing apoptosis.
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                                                                                                                    a synergistic combination of death domain receptor ligands enoid triepoxides for killing of tumour cells .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
                                                                                                                                                         Disclosure; Column 23-28; 20pp; English
 990S-149989P
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Matches 1367; Conservative
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P-PSDB; AAU75064.
                                                  Rosen GD, Kao P;
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                                                                                                                                                                                                                                                                                                                 Partial amino acid sequences were determined for the 55 and 75kD TNF-BPB (see AAR11072-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda 9t11. Positive clones were identified and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved TNF-binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 2111;
                                                                                                                                                                                                                                                 Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody prodn.
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Pred. No. 0;
0; Mismatches
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     Location/Qualiflers
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/*tag* a
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                                                                                                                                    90CH-0001347,
89CH-0003319,
90CH-0000746,
                                                                                                                                                                           (HOFF ) HOFFMANN-LA ROCHE AG
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Best Local Similarity 99.9%;
Matches 1366; Conservative
                                                                                                                  90EP-0116707
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                                                                                                                                                                                                                             WPI; 1991-081851/12.
                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ10956.
                                                                                                                                                                                                                                      P-PSDB; AAR11082
                                                                                                                                                                                               Brockhaus M,
Schlaeger EJ:
                                                                                                                                    20-APR-1990;
12-SEP-1989;
08-MAR-1990;
                                                                                                                  31-AUG-1990;
                 sig_peptide
                                    mat_peptide
                                                                                              20-MAR-1991
                                                                           EP417563-A.
                                                                                                                                                                                                         Schlaeger
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Expression of this receptor is regulated by shedding of the
extracellular receptor fragment. The p55 TNF-R can be shed in response
to different inducing agents, e.g. phorbol myristate accette (PMA),
depending on cell type. The only region of the receptor whose structure
affects the shedding response is the spacer region (see AAR75012) in the
extracellular domain. This region is located close to a site of cleavage
of the molecule, and links the Cys rich module to the transmembrane
continuers between human p55 TNF-R and murfine epidermal growth factor
contempers between human p55 TNF-R and murfine epidermal growth factor
contempers between human p55 TNF-R and murfine epidermal growth factor
contempers between human p55 TNF-R and murfine epidermal growth factor
contempers between human p55 TNF-R and murfine epidermal growth factor
contempers between human p55 TNF-R and murfine substitutions
(AAR75026-47). Of the spacer region, the most important of these.

CR ANT5026-47). Of these residues, with the interpedence of a limited
contempers on the identity of these residues, with alter the
conformation of the protein adversely effect the shedding process. The
murations shown in AAR75013-47 were introduced in order to create an
conformation of a protease that is capable of cleaving the soluble TNF-R
from the cell bound TNF-R.
conformation of a protease that is capable of cleaving the soluble TNF-R
from the cell bound TNF-R.
conformation of the protein margines and protease
conformation with the transmembranes of these inhibitors can be seen in
                                                                               p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera; epidermal growth factor receptor; EGF-R; protease; inhibitor; phorbol myristate acetate; PMA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protease capable of cleaving soluble tumour necrosis factor (TNP) receptor - from cell-bound TNF- receptor, useful for antagonising deleterious effects of TNF.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function.
                                                                                                                                                                                                                                                  "possible poly.A signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used for enhancing TNF
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                                                                                                                                                              Location/Qualifiers
256..1623
/*tag= a /*tag=
product p55 TNF-R
2143..2149
/*tag= b
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                           19-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Batkin M, Brakebusch C,
                                                                                                                                                                                                                                                  /note-
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P-PSDB; AAR75084.
                                                      p55 TNF-R gene.
                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA
                                                                                                                                                                                                                                                                                                                                  11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                            12-0CT-1993;
                                                                                                                                         Homo sapiens
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AAQ90513;
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1095 1155 1215 1020 1080 1035 240 900 960 435 495 300 555 360 615 420 675 480 735 540 600 855 999 915 720 975 780 840 316. GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAAAGAGA GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCAACCCCCTTCAGAAG GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA GATAGTGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC TGCAGGGAGTGTGAGAGGGGCTCCTTCACCATCAGAAAACCACCTCAGACACTGCCTC AGCTGCTCCAAATGCCGAAATGGGTCAGGTGGAGATCTCTTGCACAGTGGAC CGGGACACCGTGTGTGCGCTGCAGGAACCAGTACCGGCATTATTGGAGTGAAAACCTT CGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT TICCAGIGCTICAATIGCAGCCTCIGCCICAAIGGGACCGIGCACCICTCCIGCCAGGAG TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACAAGTTGTGCCTACCCCAGATTGAG **AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT** TCCAAGCTCTACTCCATTGTTGTGGGAAATCGACACCTGAAAAGAGGGGGAGCTTGAA GGAACTACTACTAGCCCCTGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGGGGCACCACCCTATCAGGG TGGGAGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTAC 1276 1081 1336 셤 ö

> . 0 2; Indels Score 1364.8; Pred. No. 0; 0; Mismatches Ouery Match Best Local Similarity 99.9%; Matches 1366; Conservative (

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ha is involved as a
autoimmune diseases
                                                        Length
useful for treating diseases where TNF alpha is involved
                                                                          3; Indels
                                    Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T; 0 other;
          causative agent, e.g. cachexia, sepsis and autoimmune specifically rheumatoid arthritis. See also AAQ20974.
                                                        DB 13;
                                                       Score 1363.2;
Pred. No. 0;
                                                                          0; Mismatches
                                                      99.68;
99.88;
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Matches 1365; Conservative
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                                                                                          CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCG
                                             The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gtil using a probe (AAQ20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is
                                                                                                                                                                                                                                                                                                                                                                                                                            extracellular domain of human
                                                                                                                                                                                                                                                             Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss; extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis
                                                                                                                               CTTTGCGGCCCCGCCCTCCCGCCCGCCCAGTCTTCTCAGATGA 1368
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/note- "homologous to probe AAQ20974"
242..751
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encodes the extrace TNF alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brennan F;
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
155..1522
155..274
155..274
/*tag b
/*tag c
4/3..532
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                                                                                                                                                                                                                                             TNF-alpha binding protein gene.
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                                                                                                                                                                                      AAQ20973 standard; DNA; 2062
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P-PSDB; AAR20787.
                                                                                                                                                                                                                                                                                              Homo sapiens
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This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA library in gt10 was screened with probe AAQ29236. Ten hybridising clones were plaque purlified and cDNA size determined by PAGE against an ECO RI digested phage DNA. The liserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha scquenced. The coding region of the majority of the human TNF-alpha action, and cloned into a mammalian cell expression vector, resulting in prTNRR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane engineering a termination codon just prior to the transmembrane restriction fragment which was cloned into prTNRR, giving pTNFRecd. DNA sequencing confirmed this contained the designed DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 ArgGCCCrCrCcACCGrGCCrGACCrGCrGCrGCrGGrGCrCcrGGAGCrGrrGrG 214
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                                                                                             New polypeptide capable of binding human TNP alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;
                                   Gray PW, Turner MJC;
                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1363.2;
; Pred. No. 0;
0; Mismatches
           SUNLEY RES CENT
                                                                                                                                             Claim 4; Fig 1; 43pp; English.
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Best Local Similarity 99.8%;
Matches 1365; Conservative
                                  Feldmann M,
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P-PSDB; AAR24000.
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                                 Brennan FM,
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                    CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGCG 1320
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                                                                                                                                                                  TGGGAGGACAGCCCCACAGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; pulmonary diseases; septic shock; HIV infection; AIDS; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                   CTTTGCGGCCCCGCCCTCCCGCCCGCCCAGTCTTCTCAGATGA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour necrosis factor alpha; extracellular binding domain;
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/product- human TNF-alpha
1265.1267
/*tag- b
/note- 33
1265.1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq: "GAC", aa: Asn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Encodes TNF-alpha 55kD receptor.
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1258..1260
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/codon= Sex
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/*tag= f
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The Tumour Necrosis Factor Binding Protein I is the soluble form of type I TNF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency. See also AAQ1212-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type T TNF receptor or soluble domain
                                                                          /*tbg-
319..864
/*tag= d
/label= soluble_domain
/note= "may be 2 codons shorter or a few codons
longer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;
 te= "in-frame termination codon"
..1620
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/note= "TBP-I derived sequence"
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/note= "TBP-I derived sequence"
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/product- type I TNF receptor
256..318
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/label- transmembrane_domain
885..504
/*tag- i
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'note= "TBP-I derived
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89IL-0092697
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/*tag= 1
/number= 4
2145.2150
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/*tag= c
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634..756
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P-PSDB; AAR12550.
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13-DEC-1989;
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  TGGGAGGACCCCCACACAGCCACAGAGCCTAGACATGATGACCCGGGACGCTGTAC 1080
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                               AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
                                                                                                               GGAACTACTACTAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC
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/*tag= a
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GCCCCTCCACCGTGCCTGACCTGCTGCTGCCCCTGCCCCTGCCCCTGCCCTGCCCTGCCCTGCTG	CTGGTGCTCCTGGAGC	CAAATAATTCGATTT CAAATAATTCGATTT CCAGGCCGGGGCAGC CCAGGCCCGGGGCAGC CCAGGCCCGGGGCAGC CCAGGCCCGGGGCAGC CCAGACCCCCCCGGGCAGG	GAAACCACCTCAGA GAGATCTCTTCTCCA GAGATCTCTTCTTCCA GAGATCTCTTCTTCCA CGGCATTATTGGAGTC [TTTCTAAGAGAAACG TTTCTTAAGAGAAACG TTTCTTAAGAGACACG AAGTTGTGCCTACCCC TIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TTCAGTCCCACTCCAG TTCAGTCCCACTCCAG TTCAGTCCCAGTCCAG TTCACCTCCAGCTCCAG TTCACCTCCAGCTCCAG TTCACCTCCAGCTCCAG TTCACCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCCCCCCC
ATGGGCCTCTCACCGTCCTG ATGGGCCTCCCCCGTCCTG GGAATATACCCCTCAGGGGTTA GGAGTATATCCCCTCAGGGGTTA GGATATTACCCCTCAGGGGTTA AAGTGCTGTGTCCCCAAGGAA AAGTGCCACAAAGGAACCTACT TGCAGGGAGTGTGTGAGAAGGCGCT TGCAGGGAGTGTGTGAGAGCGCT TGCAGGGAGTGTGAGAGCGCT TGCAGGGAGTGTGAGAACCTACT TGCAGGGAGTGTGAGAGCGCT TGCAGGGAGTGTGAGAGCGCT TGCAGGGAGTGTGAGAGCGCT TGCAGGGAGTGTGAGAACCTACT TGCAGGGAGTGTGAGAGCGCT TGCAGGGAGTGTGAGAAACCTACT TGCAGGACACCGTGTGAGCCCT TGCAGGACACCGTGTGAGAAAA TCCAGTGTTGATTTTTTTCAGCCCT TCCAGTGTTTTTTTTTT	ACCTGCTGCTGCCA 	AATATATCCACCCT AATATATCCACCCT AATATATCCACCCT TGTACAATGACTGT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCTTCACCGCTTCA AATGGGTCAGGTG AAATGGGTCAGGTG AAATGGGTCAGGTG AGAAGAACCAGTAC 	3CCATGCAGGTTTC [1111111111111111111111111111111111	DECCRAACCCAAGC
	CTCCACCGTGCCTGJ 	GTGTGCCCCAAGGAA HIIIIIIIIIIII CACAAAGGAACCTACTT CACAAAGGAACCTACTT CACAAAGGAACCTACTT CACAAAGGAACCTACTT GAGTGTGAGAACGCCCC	3364746464666677 TCCAAATGCCGAAGG TILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	MGAACACCGTGTGCACCTT MAAACACCGTGTGCACCTT MAACACCGTGTGCACCTT MAGTAACTGTAAGAAACTTAAGAAACTTAAGAAACTTAAGAAACTTAAGAAACTTAAGAAACTTAAGAAACTTAAGACTTTATTATCCCTCCTTTTATCCTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTATCCTTCCTTTTTATCCTTCCTTCCTTTTTATCCTTCCTTTTTATCCTTCCTTTTTATCCTTCCTTTTTATCCTTCTT	CTACTACTAAGCCCTGGG CCTGGGCTTCAGTCCGG CCCTGGGCTTCAGTCCGG CCTGGGCTTCAGTCCGG GTGACTGTCCCAACTTGC GTGACTGTCCCAACTTGC GTGACTGTCCCAACTTGC GTGATTGCTTGCAACTTGCGAACTGCGAACTGCGAACTGCGAACTGCAACTTGCAACTTGCAACTGCAACTGCAACTGCAACTGCAACTGCTGCCAACTGCTGCAACTGCTGCAACTGCTGCAACTGCTGCAACTGCTGCAACTGCTGCAACTGCTAGTGCTAGTGCTTGCCAACTGCTAGTGCTTGCCAACTGCTAGTAGTGCTAGTAGTGCTAGTGCTAGTGCTAGTAGTGCTAGTAGTGCTAGTAGTGCTAGTAGTGCTAGTGCTAGTAGTGCTAGTGCTAGTAGTGCTAGTAGTGCTAGTAGTGCTAGTAGTAGTGCTAGTAGTGCTAGTAGTGCTAGTAGTGCTAGTGCTAGTAGTGCTAGTGCTAGTGCTAGTAGTGCTAGTAGT

Search completed: June 8, 2003, 23:42:11 Job time : 348 secs

June 8, 2003, 22:32:19 ; Search time 3520 Seconds (without alignments) 11310.409 Million cell updates/sec 4109280 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0
Maximum DB seq length: 2000000000 US-09-899-422A-1 1368 GenEmbl:* Title: Perfect score: Scoring table: Database : Sequence: Searched: Run on:

38: em_sy:* 39: em_htgo_hum:* 40: em_htgo_mus:* 41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	A29098 Synthetic D M63121 Human tumor BC010140 Homo sapi M33294 Human tumor A26412 cDNR for (5 AX409713 Sequence AX6412 cDNR for (5 AX409713 Sequence AX9313 H.saplens TA806330 Sequence AX9313 H.saplens TA8041076 Sequence AX9907 Synthetic n A21522 TNF alpha g 143805 Sequence AX0255 55kD recept AX03337 Rettus no AF32997 Rattus no AF32998 Rattus no AF32998 Rattus no AF32998 Rattus no AF32998 Rattus no AF32999 Mus musculu X57796 Mouse mRNA U90937 Bos taurus AX03337 Sequence BN00974 Sequence AX13408 Sequence AX13408 Sequence AX13408 Sequence AX13408 Sequence AX1525 oligonucleo	from patent EP0393438. from patent EP0393438. r-Fogy, I. and Stratowa, C. iin and DNA coding therefor 1990: NNAL G.M.B.H
SUMMARIES	A29098 HUMINER A26412 AX409713 AX409713 AX409713 AX409713 AX309713 A43873 A43873 A43873 A43873 A43873 A43873 A43873 A21522 A20255 A20255 A20255 A20255 AX025094 AX132997 AX132997 AX132997 AX132997 AX132997 AX1323997 AX1323999 AX1323998 AX13239	68 bp otor faure orote OCT-
Length DB	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A29098 136 A29098 229098 136 A29098 1 GI:1248892 synthetic construct. synthetic construct artificial sequences, 1 (bases 1 to 1368) Hauptmann, R., Himmler, A., P. Hauptmann, R., Himmler, A., P. Patent: EP 039438-A 48 24, BOEHRINGER INGELHEIM INTERN
% Query e Match	6668 44444444444444448 888 84444448 888 444444	A29098 Synthetic D A29098.1 G A29098.1 G Synthetic c synthetic c synthetic c synthetic c synthetic synthetic Thref TNF-recepto PAF-recepto PAF-recepto PAF-RECEPTO PAF-RECEPTO PAF-RECEPTO PAF-RECEPTO PAF-RECEPTO PAF-RECEPTO
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2194 bp mRNA linear PRI 12-JUL-2001.

Homo sapiens, tumor necrosis factor receptor superfamily, member
1A, clone MGC:19588 IMAGE:4131360, mRNA, complete cds.
BC010140
MGC.
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"Intp://www.nisc.nih.gov/
Contact:
"Insc_mgc@nhgri.nlh.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                    found
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg.R.
Direct Submission
Submitted (02-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                               GCTGACCCCATCCTTGGGCAGCCTCGCCTCGGACCCCATCCCCAACCCCTTCAGAAG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site:
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Mammalia, Eutheria, Primates,
1 (bases 1 to 2194)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Homo sapiens
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/gene="TNF receptor"
294. .1571
/gene="TNF receptor"
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1 (bases I to 2087).
Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.L.; Rice, G.C.; Wong, G.H.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J. and Goeddel, D.V.
Molecular cloning and expression of a receptor for human tumor negrosis factor.
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//protein_id="aahi0140.1"
//protein_id="aahi0140.1"
//dlxref="di:14603368"
//translation="micstydpictrollepitudeilygivpsgylgicyphicberedscoperations"
POGKYIHPONNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHILRHCLSC
SKOKKRAGQYELSSCTYDRDTVGGRKROYRHWABENLEOFERKSICLINGTVHILSCQE
KQNTVGTCHAGFFLENEDCSGSNCKKSLECTKLCLPOIENYRGTEDSGTTVLIPLVI
FPGLCLILSILFIGIMYRYQRMKSKLYSIVGKSTPEREGGELGTTTKPIAPNPSFSPT
POGTPTLGCRSPVPSSFYFFSSTYTPGDCPNFARRAYPPGGADPTITATALASDPI
PNPLORWEDSAHKPGSLJTDDATLYAVPREVPPLRMEFYRRIGILEITATALASDPI
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Series: IRAL Plate: 27 Row: m Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 339755.
Location/Qualifiers
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                                                          /organism="Homo sapiens"
/db_xref="LocusID:7132"
/db_xref="taxon:9606"
/clone="MG:19588 IMAGE:4131360"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/nab_host="nH108-R"
/note="Vector: pOTB7"
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A26412 2111 bp DNA linear PAT 26-APR-1995 CDNA for (55kD TNF-BP) tumor necrosis factor binding protein from patent EP0417563.
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Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and Schlaeger,E.J.
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Patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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//db_xref="fg1:339745"
//db_xref="g1:339745"
//translation="MGLSTVPDLLLPUVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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GRCLREAQYSMLATWRRTPRREATLELLGRVLRDMDLLGCLEDIEBALCGPAALPPA
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Draft entry and computer-readable sequence for [1] kindly submitted
by T.Schall, 26-WAR-1990.
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="tumor necrosis factor receptor"
/codon_start=1
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Sequence 2360 from Patent WO0229103.
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PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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FFGLCLLSLLFIGLMYRYQRMKSKLYSIVCGKSTPRREGELEGTTTKFLAPNFSFSPF
PGFPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYGADPILATALASDPI
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Pred. No. 2.1e-265;
0; Mismatches 1;
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/product="55 kD TNF-BP"
/protein_id="CAA01805.1"
/db_xref="G1:904969"
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milarity 99.9%;
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POGRY IHPONNSICCTRCHRGTYLXNDCPGFGODTOCRECESGSFTASENHIRHCISC
SKORKEMGGVEISSCTVDTVGGCRRNQYRHYWSENLFQCFNCSICLNGTVHISCOE
KQNTVCTCHAGFFLENECVSGSKOKKSLECTRICLPOIENVRGTEBSGTTVLLPLVI
FFGLCLLSILEIGLAYRYQRMKSKLYSIVGGKSTPEREGELEGTTTRFLAPNESFPT
PRGTPFLIGSSPYPSSTFTSSSTYTPGCCPNPRAPRRRYAPPYGGADPITATALIANDPI
PNPLQKWEDSAHKRGSLLYDDPATIYAVPREVPPLRWKEFYRKLGSDHEIDRIELQH
GRCIREAQYSMLATWRRTPRREATLEILGRVLRDMDLIGGLEDIEERLCGFPALPRA
                                                                                                                                                               Homo sapiens tumor necrosis factor receptor mRNA, complete cds. M58286 M33480 M58286.1 GT:339753
             1260
                                                               Homo spijens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Manmalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2111)
Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M.,
Tabuchi, H. and Lesslauer, W.
Molecular cloning and expression of the human 55 kd tumor necrosis
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                                                                                                          /product="tumor necrosis factor receptor"
/protein_1d="AAA36753.1"
/db_xref="GI:339754"
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Pred. No. 2.1e-265;
3; Mismatches 1;
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Human cell line HL60, cDNA to mRNA.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HL60"
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/gene="TNF receptor"
274. .1551
/gene="TNF receptor"
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187. .1554
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                    GATAGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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/product-*tumor necrosis factor receptor type 1*
/product-*tumor necrosis factor receptor type 1*
/db_xref-*G1:3724*
/db_xref-*SWISS-PROT:P19438*
/db_xref-*SWISS-PROT:P19438*
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/translation-*MGISTYPDILLEPUTLELLYGIYPSGSSFTASENHLRHCLSC
SKCRKEMGQVEISSCTYDRDIVGGCRRNQYRHYWSENLFQCFNCSLCINGIYHLSCQE
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FFGLCLLSLLFIGLMYRYQBWKSKLYSIVCSKSTPRREGELEGTTTRFLAPNESFSPT
PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYGADDILATALASDPI
PNPLCXWEDSAHKFOSLDTDPATLYAVVENYPPLRWKEFVRRLGLSDHEIDKLELCN
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Pred. No. 2.1e-265;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
256..2161
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Soluble forms of tumor necrosis fare the type I TNF-R, cloned using soluble form, encodes both the celthe receptor EMBO J. 9 (10), 3269-3278 (1990) 1698610
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/gene="TNF-R"
256. .1623
/gene="TNF-R"
/codon_start=1
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Nophar, Y., Kemper, O., Brakebusch, C., Englemann, H., Zwang, R., Aderka, D., Holtmann, H. and Wallach, D.
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FEATURES Location/Qualifiers 1. 2175 Source 1. 2175 /Organism="unidentified" /db_xref="taxon:32644" BASE COUNT 474 a 641 c 604 g 456 t ORIGIN	Ouery Match 99.9%; Score 1366.4; DB 6; Length 2175; Best Local Similarity 99.9%; Pred. No. 2.1e-265; Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGCTCCTGGAGCTGTTGGTG 60	### ##################################	316 GGAATATACCCTCAGGGGTTATTTTTGGACTGGCCCTCAGGGGACAGGGAAAGAA 375 121 GATAGTGTGTCCCCAAGGAAATATACACCTCACCTCAAATAATTGGATTTGCTGTACC 180	376 GATAGTGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435 181 AAGTGCCAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGGGGG	241 IGCAGGGGTGTGAGGGGCTCCTTCACGGCTTCAGAAAACCACCTCAGACACTGGCTC 300		616 CGGGACACCGTGTGTGGCTGCAGGAGAACCAGTACCGGCATTATTGGAGTGAAAACTT 675 421 TTCCAGTGCTTCAATTGCAGCCTCTGCTCAATGGGACCGTGCACTCTCTGCCAGGAG 480 111111111111111111111111111111111111	481 AAACAGAACACCGTGTGCACCTGCCAGGTTTCTTTCTAAGAAAACGAGTGTGTC 540	796 TCCTGTAGGAAAAAAGCCTGAGGAGTGCACGAAGTTGTCCCCCCCC	661 GGTCTTTGCCTTTTATCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG 720		841 CCCACCTGGGCTTCACTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900
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241 TGCAGGGAGTGTGAGAGCGCTCCTTCACCGCTTCAGAAACCACCTCAGACACTGCCTC 300 [11111111111111111111111111111111111		721 TCCAAGCTCTACTCCATTGTTTGTGGGAATCGACCTGAAAAAGAGGGGGAGCTTGAA 780	1021 TGGGAGGACAGCCCAAAGCCACAAGACCTGAACACGATGACCCGGACGCTGTAC 1080 1276 TGGCAGGACAGCGCCCAAAGCCACAAGACCTGAACACTGATGACCCCGCGACGTTAC 1335 1276 TGGCAGGACAGCGCCCAAAGCCACAGAGCATGACCCCGCGCGACGTGTAC 1335 1081 GCCGTGGTGGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGCCTG 1140 11316 GCCTGGTGGAACGTGCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGCTG 1395 1141 AGCGACCACGAGAACGTGCCCCGTTGCGCTGGAACGGCGCTGCGGCGCCTAGGCTG 1395 1141 AGCGACCACGAGAACGTGCCCCGTTGCGCTGCAACGCGCGCG
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Search completed: June 9, 2003, 01:12:25 Job time : 3526 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

June Run on:

9, 2003, 01:12:29; Search time 1566 Seconds (without alignments) 4705.585 Million cell updates/sec

US-09-899-422A-2 Title: Perfect score:

2487 1 MGLSTVPDLLLPLVLLELLV......DIEEALCGPAALPPAPSLLR 455 Sequence:

BLOSUM62 Scoring table:

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16154066 seqs, 8097743376 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line

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em_estfun:* b_est3; gb_est4 gb_est5

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em_gss_other:* em_gss_pro:* em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AGENCOURT_8489850 Lupski_dorsal_root_ganglion Homo sapiens CDNA clone IMAGE:6184295 5', mRNA sequence. BQ723672.1 GI:21862569 BQ723672 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BQ723672

Homo sapiens ORGANISM

human.

REFERENCE AUTHORS TITLE

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 931)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

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/tissue_type="T_calls from T_call leukemia"
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was primed with a Noti-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 957)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Unpublished (2001)

Contact: Genoscope
                 178 GluCysValSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuPro
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13573 row: d column: 24
High quality sequence stop: 607.
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Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

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Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Agencurt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

Plate: LLAM12803 row: b column: 06

High quality Sequence stop: 77.

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Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Bomo.

1 (bases 1 to 741)

8 NIH-MGC http://mgc.ncl..nih.gov/.
National institutes of Health, Mammallan Gene Collection (MGC)

14 Unpublished (1999)

15 Contact: Robert Strausberg, Ph.D.
Email: cgaphs-remail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC. Clone distribution information can be found through the I.N.A.G.E. Consortium/Libra at:

Location/Qualifiers

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                                AlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeuGLuGGlyArgVal
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240 LysSerLysLeuTyrSer----IleValCysGlyLysSerThrPro---GluLysGlu 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yama, Kilsarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3986
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/clone_11b-"NT2RP3"
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1 (bases 1 to 942)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 974)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.infl.gov

Tissue Procurement: DCTD/Drp

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Theyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Http://mage.linl.gov

Plate: LLAM10185 row: g column: 20
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/db_xref="taxon:9606"
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/clone="type="foliate to the prime to the not I and coloned into the Not I and Eco RV sites of the prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.

a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filiangth.invitrogen.com"
http://fulllength.invitrogen.com"
a 258.c 259 g 221 t 6 others
                                                                                                                                                                                                                                                               AL577008 LT_NFLO06_PL2 Homo saplens cDNA clone CSODI082XA01 5 prime, mRNA sequence.

AL577008.1 GI:12939716
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                                                                                           uAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePh 220
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           180 lSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGl
                          LysGlnAsnThrValCysThrCysHisAlaGly-PhePheLeuArgGluAsnGluCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Onpublished (2001)
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// Organism="Homo sapiens"

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/organism="Homo:9606"

/clone="IMAGE:531041"

/clone="Lib="NHIE MGC_71"

/tissue_type="leiomyosaccoma"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
L (bases 1 to 994)
L Unpublished (1999)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Likr at:
http://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                 994 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041
5', mRNA sequence.
                                      CTTTTGCCTTTTATTCCTCTTCAGTGGCGTAAATGTAGTCGCTGCCACGCGGAAGCC 719
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                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="NIH-MGC_019"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tisb_host="PH108 (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb Library enriched for full -length clones and constructed by Life Technologies.
Note: this is a NIH_MCC Library."
9 a 265 c 265 g 185 t
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Matches:
Conservative:
Mismatches:
Indels:
quality sequence stop: 657 Location/Qualifiers
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Best Local Similarity:
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        Contact: Taked 1sogai

Contact: Taked 1sogai

Genomics Laboratory

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Tel: 81-438-52-3976

Tel: 81-438-52-3976

Email: genomics@thitco.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
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                                                                                                                  1..889
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Catarrhini; Hominidae; Homo.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Zamamoto,J., Wakamatsu,A., Nakamura,Y.; Nagai,T., Sugano,S. and
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                                     AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr
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Homo sapiens cDNA clone HEMBA1001229
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41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]			ATGAGCATCTTAGGGGCACCTCAGGGCACCCCAGTGCTTTTGCCCTGGTC IlePhePhe-GlyLeuCysLeuLeuSerLeuLeuPheileGlyLeuWetTytArgTyrGl :::	BG680679 718 L 602626965F1 NCI_CGAP_Skn4 Home mRNA sequence. BG680679 BG680679.1 GI:13912076 EST. human. Homo sapiens	MEHZZDUME	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	a & a & a	6 8 8 8 8 8	6 6 6 6 6	RESULT 13 BG680679 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES
Oy 423 ArgValLcuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAlaLeuCys 442	z s	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 916) AUTHORS NIH-MGC http://mgc.ncl.nih.gov/. TITLE National Institutes of Health, Mammallan Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution incom be found through the I.M.A.G.E. Consortium/LLNL, at:	http://image.llnl.gov Plate: LiAM1500 row: f column: 06 High quality sequence stop: 827. FEATURES Location/Qualifiers 1. 916 /organian="Momo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5199749" /clone=lib="NIH_MGC_114" /lab_host="Mortan" html" /note="forman" html" /note="forman" html"	Site_2: Ecorv (destroyed); RNA source anonymous pool of male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library." BASE COUNT 204 a 261 c 243 g 208 t		US-09-899-422A-2 (1-455) x BI757305 (1-916) Oy MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuLeuVal 20

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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life a rechnologies. Note: this is a NCI_CGAP Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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                                                                                                                                                                                                                        Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: C column: 12
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Matches:
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Mismatches:
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Unpublished (2002)
Contact: Kim YS
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                   ArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisGluIleAspArgLeuGlu
                                                                                                                                                                                                                                                                                                        prime, mRNA sequence.
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212
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                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                     4.97e-104
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June Run on:

8, 2003, 22:41:48 ; Search time 92 Seconds (without alignments) 4560.150 Million cell updates/sec

US-09-899-422A-1 1368 1 atgggcctctccaccgtgcc......cgcccagtcttctcagatga 1368 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

441362 seqs, 153338381 residues Searched:

Total number of hits satisfying chosen parameters:

882724

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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~	1366.4	66.66	2161	4	US-09-505-250-3	m
m	1366.4	99.9	2175	-	US-08-321-668-1	-
4	1366.4	99.9	2175	Н	US-08-837-941-1	Sequence 1, Appl1
2	1366.4	6.66	2175	Н	US-08-126-016-1	Ä
ဖ	1366.4	6.66	2175	4	US-08-054-970-1	ï
7	1360	99.4	2062	Н	US-08-050-319B-24	24
œ	1360	99.4	2062	7	US-08-465-982-24	24,
6	690.4	50.5	1956	7	US-08-762-308-10	_
9	685.4	50.1	2440	4	US-09-513-007-1	1,
11	632.8	46.3	9689	~	US-08-627-151A-6	ی ا
12	632.4	46.2	6889	Ч	US-08-286-740-2	N
13	632.4	46.2	6889	Ŋ	PCT-US95-09576-2	'n
14	593.6	43.4	9	-	US-08-050-319B-47	47,
13	593.6	43.4	9	~	US-08-465-982-47	47,
16	515.4	37.7	1478	4	US-09-149-922-6	9
17	514	37.6	1301	4	US-08-804-166-7	Sequence 7, Appli
18	514	37.6	1301	7	US-08-910-991-7	7
13	206	37.0	1147	4	US-08-804-166-5	Sequence 5, Appl1
20	206	37.0	1147	4	US-08-910-991-5	'n
71	501.4	36.7	504	Н	US-08-050-319B-56	56,
77	501.4	36.7	504	7	US-08-465-982-56	Sequence 56, Appl
23	499.4	36.5	501	7	US-08-050-319B-1	1, 4
24	499.4	36.5	501	7	US-08-465-982-1	1,
25	483	35.3	483	4	US-09-326-394-1	7
26	424.4	31.0	1049	7	US-08-804-166-1	Sequence 1, Appli
23	434.4	31.0	1049	7	US-08-910-991-1	'n

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61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120

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50.00	Sequence 3, Appli Sequence 3, Appli Sequence 49, Appl Sequence 49, Appl Sequence 236, Appl	Sequence 3, Appliance 51, Appliance 51, Appliance 51, Appliance 11, Appliance 9, Ap	Sequence 1, Appli Sequence 3, Appli Sequence 14, Appl Sequence 13, Appl
US-08-804-166-3 US-08-910-991-3 US-08-050-319B-53 US-08-465-982-53	0.08-0.03-0.03-0.03-0.03-0.03-0.03-0.03-	US-08-050-319B-51 US-08-050-319B-51 US-08-928-069-11 US-08-828-683A-9	US-08-815-469-1 US-08-815-469-3 US-08-232-463-14 US-08-804-227C-13
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ALIGNMENTS

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1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
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99.9%; Score 1366.4; DB 3; Length 2161;
Best Local Similarity 99.9%; Pred, No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0;
                                  Sequence 1, Application US/09106038A
Fatent No. 6007995
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowsert
ITILE OF INVENTION: ANTISENSE MODULATION OF INFII
ITILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1515 Pharmaccuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
STREET: Ca.
COUNTY: U.SA.
ILLE OF UND STREET: CA.
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWAR:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REJESTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECOMMUNICATION INFORMATION:
TELEPRAX: (760) 503-3820
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-09-106-038A-1
RESULT 1
US-09-106-038A-1
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                                                         GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA
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APPLICANT: ROSEN, Glenn
APPLICANT: RAO, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Tripcolides and Death Domain Ligands
TITLE OF INVENTION: Tripcolides and Death Domain Ligands
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT PILING DATE: 2000-02-15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                         Score 1366.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                     Sequence 3, Application US/09505250A Patent No. 6329148 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         96.98;
99.98;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: H. sapiens
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Best Local Similarity
Matches 1367; Conserv
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           1201
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                   GATAGTGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
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                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1366.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
APPLICATION WIMBER: US/08/321,668
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-007-1993
ATORNEY AGENT INFORMATION:
RAME: BROWD, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMULICATION INFORMATION:
TELECHONE: 202-628-5197
TELEFRAX: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.9%;
Matches 1367; Conservative (
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
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256..1620
   CORRESPONDENCE ADDRESS
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; LOCATION:
US-08-321-668-1
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                  GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG
 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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Patent No. 5665859
Patent No. 566589
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WALCH, David
APPLICANT: VARFOLOMER', Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE THE THE RECEPTORS, THEIR PREPARATION AND THEIR INDMERS OF SEQUENCES: 42
                                                                                                                                       CTTTGCGGCCCCGCCCTCCCGCCCGCCCCGTTTCTCACATGA 1368
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IITLE OF INVENTION: THE THE TRECEPTORS, THEIR PREPARATION AND THEIR USE NUMBER OF SEQUENCES: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CONFUTER: Eloppy disk

CONFORTER: PER PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DARA:

APPLICATION NUMBER: US/08/837,941

FILING DATE: 28-APR-1997

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                    ADDRESSE: BROWL AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1366.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-007-1994
APPLICATION NUMBER: II 107268
FILING DATE: 12-007-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELECHOME: 202-628-5197
TELECHAN: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                            TELEX: 202-/3/--
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDENESS: single
STRANDENESS: lingle
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99.98;
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Best Local Similarity 99.9
Matches 1367; Conservative
               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 256..1620
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                                       AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
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                                                                              TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, COTC
APPLICANT: VARPOLOMEDV, Eugene
APPLICANT: WALSHIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

Sequence 1, Application US/08837941 Patent No. 5766917

RESULT 4 US-08-837-941-1

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256 ArGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
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APPLICANT: ENGELMANN, HARTWUT
APPLICANT: BRAKBBUSCH, CORD
APPLICANT: ADERKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: RECROSIS FACTOR BINDING PROTEIN I (TBP-I)
NUMBER OF SEQUENCES, 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdv nr.
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                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                     E: Browdy and Nelmark
419 Seventh Street, N.W., Suite 300
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGER L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECHONE: 202-628-5197
TELECHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                         WALLACH4
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99.98;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
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STRANDEDNESS: single
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LOCATION:
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US-08-126-016-1
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                    STREET:
                                                                                                                                                                CITY:
STATE:
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Best Local 9
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                                                                                            TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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                                       TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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Patent No. 5811261
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WALLACH, DAVID
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Sequence 1, Application US/08054970 Patent No. 6395267
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGIGTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.9%;
Matches 1367; Conservative 0
                                                                                                                                                                                                                                                                                                                            TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 256..1620
                                         GENERAL INFORMATION:
  RESULT 6
US-08-054-970-1
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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FLING DATE: 03-MAY-1993
CLASSIFICATION: 435 APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TILLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: score 1366.4; Pred. No. 0; 0; Mismatches AUDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA

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Sequence 24, Application US/08050319B

RESULT 7 US-08-050-319B-24

120 240 180 300 360 274 334 394 214 395 TGCAGGGGAGTGTGAGAGCGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 454 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420 574 9 335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 241 TGCAGGGAGTGTGAGAGCGCCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTCCTGGAGCTGTTGGTG AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGCACAGTGGAC Gaps ö 1; Length 2062; GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TWFalpha (Tumor
TITLE OF INVENTION: Medicial Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS: SOFTWARE: PatentIn Release #1.0, version #1.25 SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993 CLASSIFICATION: 435 B Pred. No. 0; 0; Mismatches 99.4%; Score 1360; 99.6%; Pred. No. 0; ATTORNEY AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 517-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24: Eloppy disk IBM PC compatible E: Reed & Robbins 635 Bryant Street MOLECULE TYPE: CDNA to mRNA FEATURE: 2062 base pairs SEQUENCE CHARACTERISTICS: Conservative TYPE: nucleic acid STRANDEDNESS: double CDS 155.,1519 STREET: 635 Bryant CITY: Palo Alto STATE: California linea Query Match Best Local Similarity Matches 1363; Conserv USA ADDRESSEE: NAME/KEY: ; LOCATION: US-08-050-319B-24 COUNTRY: LENGTH: 455 61 361 301 ద ò 윰

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AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 394
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                                                                                                                                                         COMPUTER: F.LOPY GISK
COMPUTER: F.LOPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE:
ILING DATE:
ILING DATE:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECAMMICATION INFORMATION:
TELECAMMICATION INFORMATION:
TELECAMMICATION NUMBER: 5150-0030
TELECAMMICATION SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
LENGTH: 2062 Dase pairs
  Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
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99.4%; Score 1360; DB
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches
TITLE OF INVENTION: Modified
TITLE OF INVENTION: Necrosis
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed 6 Robbins
                                                     ADDRESSEE: Reed & Robbins
STREET: 615 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                    Floppy disk
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION: 155..1519
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GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan

Sequence 24, Application US/08465982 Patent No. 5863786

US-08-465-982-24

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CGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
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                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/762,308 FILLING DATE: 09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 690.4; DB 2;
Pred. No. 3.3e-156;
0; Mismatches 351;
                                                                                                                                                                                                                                                                      NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:335--1
                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: TX
COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 418-3000
                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 1956 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%;
                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.5'
Best Local Similarity 72.2
Matches 975; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-762-308-10
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                                               AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTTCTTAAGAGAAAAAGGAGTGTGTC
                                                                                               TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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Flavia M.
MODIFIED RECEPTORS THAT CONTINUOUSLY
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Sequence 10, Application
Patent No. 5925548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beutler,
APPLICANT: Bazzoni,
TITLE OF INVENTION:
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2000-02-25
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Best Local Similarity 71.1%;
Matches 1021; Conservative
CURRENT FILING DATE: 2000-02-
PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                      ; LOCATION: (294)...(1706)
US-09-513-007-1
                                                                                                                                          TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                    NAME/KEY: CDS
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OF USE
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Patent No. 6406907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Rehrli, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Mwangi, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FA
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
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                                                                                                                                                                      Length 2440;
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                                                                                                                                                                        Score 685.4; DB 4;
Pred. No. 5.6e-155;
                                                                                                                                                                                                0; Mismatches 326;
                                       4.0
                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO L
LENGTH: 2440
60/122,156
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1475 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTAGTTTGTACTACCCCAGATTGAG 1534
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METHOD FOR SELECTING HIGH-EXPRESSING HOST CELLS
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Pred. No. 3e-142;
0; Mismatches 2;
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Patent No. 5561053
GENERAL INFORMATION:
APPLICANT: Crowley, Craig W.
TITLE OF INVENTION: METHOD FOR SEI
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1016
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-410-8926
                                                                                                                                                                                                                                                         46.38;
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 6896 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         Best_Local Similarity 99./
Matches 634; Conservative
                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                   TELEFAX: 619-410-8928
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US-08-627-151A-6
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US-08-286-740-2
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                               GCTGACCCCATCCTTGCGACAGCCCTCCGACCCCCATCCC-5------
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               CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC
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Patent No. 5866341
GENERAL INFORMATION:
APPLICANT: STINGLIA, Dominic
APPLICANT: STINGLIA, Dominic
APPLICANT: BECHERER, Kathleen
APPLICANT: BECHERER, Kathleen
APPLICANT: STINGLIA, STEWEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: SCREENING DRUG LIBRARIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Gen-Frobe Incorporated
STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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APPLICATION NUMBER: US/08/627,151A
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92141
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"AMUTTER: IBM COMPATIBLE
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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STATE:
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Pred. No. 3.7e-142;
0; Mismatches 1;
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                                                                                                                               601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GENERATECH, INC.

TITLE OF INVENTION: METHOD FOR SELECT

TITLE OF INVENTION: METHOD FOR SELECT

TITLE OF INVENTION: METHOD FOR SELECT

TITLE OF INVENTION: ADDRESS:

ORRESPONDENCE ADDRESS:

ADDRESSEE: Generatech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00,000
798PCT
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APPLICATION NUMBER: 08/286740
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 798PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.2%;
99.8%;
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Best Local Similarity 99.8*
Matches 633; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 6889 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
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                                                                                                                                       COMFUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,740
FILING DATE: 05-AUG-1994
CLASSIFICATION NUMBER: PFLICATION NUMBER: PLING DATE:
FILING DATE: PLICATION NUMBER: PRICATION NUMBER: PRICATION NUMBER: 798
FILING DATE: ATONEMATION:
NAME: Lee, Wendy M. REGISTRATION NUMBER: 798
TELEFRATION NUMBER: 798
TELEFRATION NUMBER: 798
TELEFRAX: 415/25-1994
TELEFRAX: 910/371-7168
TELEFAX: 910/371-7168
TTYPE: nucleic acid
STRANDEDNEE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNES: double
STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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                                                                        Gaps
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                                   Length 600;
                                                                      Indels
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Patent No. 5863786
GENERAL INCERNATION:
GAPPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.W Brennan
TITLE OF INVENTION: Modified human INFalpha (Tumor TITLE OF INVENTION: Necrosis Factor Alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
                                 Score 593.6; DB 1;
Pred. No. 3.4e-133;
0; Mismatches 4;
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APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                 Query Match
Best Local Similarity 99.3%;
Matches 596; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
US-08-050-319B-47
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                TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
                                                                                                          CGGGACACCGTGTGCGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                     COMPUTE: USAC

ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODDIS, RODDIS, SOBCITA L.
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
TELECOMMUTICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELECOMMUTICATION INFORMATION:
TELEPHONE: CALS, 323-3231
INFORMATION FOR SEQ ID NO: 47;
SEQUENCE CHARACTERISTICS:
TENGENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Beldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human INFalpha (Tumor
TITLE OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed 6 Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 634
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635 Bryant Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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LOCATION:
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                                                                                                                                                                                                                                                                   Length 600;
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Pred. No. 3.4e-133;
0; Mismatches 4;
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: RODDINS, RODGETA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
RELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                 43,48;
                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                               Query Match 43.4 Best Local Similarity 99.3 Matches 596; Conservative
                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..597
US-08-465-982-47
                                                                                                                                                                                                                                                                                                                                                                                                           121
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9, 2003, 01:14:09 Search completed: June Job time: 97 secs

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9, 2003, 01:17:59 ; Search time 185 Seconds (without alignments) 342.105 Million cell updates/sec
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1 MGLSTVPDLILPLVLLELLV......DIEEALCGPAALPPAPSILR 455
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                       870385 segs, 699768693 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Command line parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
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-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
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DB	9999
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% Query Match	100.0
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Result No.	H 07 M 4

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10 US-09-880-107-2360 9 US-09-898-234-16 9 US-09-899-429A-26	US-09-792-356-16	US-10-120-397	US-10-252-408-3	us-00-868	US-09-792-356-1	10 US-09-899-422-11	US-09-899-429A-21	ns-	9 US-09-898-234-14	0.50	US-09-792-356-14	US-09-899-422-	US-00-97	US-09-899-429A-7	US-09-899-429A-1	ns-09-899-4	9A-1	US-09-899-4	US-09-756-186-7	US-09-899-429A-	0 US-09-756-186-5	60-SD	-234 - 3	US-09-899-429	US-09-792-3	US-09-882-735-1	US-09-899-422-	US-09-907-263	US-09-899-429A-	US-09-359-595-1	-09-756-186-	US-09-756-18	US-10-043-487-10	US-09-911-904-1	US-09-838-718A-	-SD	US-09-882-735
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ALIGNMENTS

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APPLICANT: Hummler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION TOWBER: 08/09/896,234
CURRENT PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1993-11-17
PRIOR PILING DATE: 1993-11-17
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PRIOR PILING DATE: 1990-04-20
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PRIOR FILING DATE: 1990-04-20
PRIOR PILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SCOTWARRE: PatentIn Ver. 2.0
SEQ ID NO
Sequence 1, Application US/09898234 Patent No. US20020155112A1
                                                                                         APPLICANT: Hauptmann, Rudolph
                                                          GENERAL INFORMATION:
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LOCATION: (1)..(87)
NAME/KEY: misc.feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc.feature
LOCATION: (606)..(633)
                                                                                                       LOCATION: (606)..(633)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion.
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Matches:
Conservative:
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Indels:
Gaps:
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Best Local Similarity:
          Homo
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TYPE: DNA ORGANISM:
                  FEATURE:
NAME/KEY: (
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Stratcwa, Christian
TITLE OF INVENTION: The
FILE OF INVENTION NUMBER: 09/792,356
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR PILING DATE: 1955-06-07
PRIOR APPLICATION NUMBER: 08/183,676
PRIOR APPLICATION NUMBER: 08/183,287
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-01-02
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720 260

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Sequence 1, Application US/09792356
Publication No. US20020183485A1
GENERAL INFORMATION:
APPLICANT: Hauptmenn, Rudolph
APPLICANT: Butvery, Ingrid
APPLICANT: Butvery, Ingrid
APPLICANT: Stratowa, Christian
ITILE OF INVENTION: The Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT APPLICATION NUMBER: US/17,639
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR APPLICATION NUMBER: 07/511,430
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SOFTWARE: Patentin Ver. 2.0

SEQ ID NO

LENGTH: 1368

LTYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS

LOCATION: (1)..(1365)

NAME/KEY: misc_feature

LOCATION: (1)..(89)..(120)

NAME/KEY: misc_feature

LOCATION: (88)..(120)

OTHER INFORMATION: extracellular proteases following secretion

NAME/KEY: misc_feature

LOCATION: (606)..(633)

OTHER INFORMATION: portion of TNF-BP pro protein cleaved by

COTHER INFORMATION: extracellular proteases following secretion

MANE/KEY: misc_feature

COCATION: (606)..(633)

OTHER INFORMATION: extracellular proteases following secretion

SOFTWARE INFORMATION: extracellular proteases following secretion
                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Sequence 1, Application US/09899422

Patent No. US2020009676a1

GENERAL INFORMATION:
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT FILMG DATE: 2001-08-21
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR PLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR APPLICATION NUMBER: 07/821,750
                                                                    LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla
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                         GlyLeuCysLeuleuSerLeuleuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys
                                               GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG
                                                                                                                  GlyThrThrTysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                                                                                                              ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr
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                                         CRGANISM: Homo saplens
CRGANISM: Homo saplens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1368)
NAME/KEY: 819_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
COTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
COTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
COTHER INFORMATION: extracellular proteases following secretion.
COTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
COTHER INFORMATION: extracellular proteases following secretion.
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NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver.
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Best Local Similarity:
Query Match:
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LENGTH: 1368
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Sequence 2360, Application US/09880107

Sequence 2360, Application US/09880107

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE PatentIn Ver. 2.1
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                                                   TYPE: DNA
ORGANISM: Homo sapiens
FETUTRE:
NAME/KEY: CDS
LOCATION: (1)..(1368)
NAME/KEY: sig_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: Attracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
OTHER INFORMATION: extracellular protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
US-09-899-422-1
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO I
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Best Local Similarity:
Query Match:
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                                            LENGIH: 1368
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                       AlaaspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial Sequence: human TNF-R in
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09898234
SPELICANT: Humler, Adolph
APPLICANT: Humler, Adolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
STILE REFERENCE: 98,385-1
CURRENT APPLICATION NUMBER: US/09/898,234
CURRENT FILING DATE: 2001-07-03
SPRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/525,998
PRIOR PILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR PILING DATE: 1995-11-17
PRIOR PILING DATE: 1995-11-17
PRIOR PILING DATE: 1999-04-20
SPRIOR RELING DATE: 1990-04-20
SPRIOR RELING DATE: 1990-04-20
SEQ ID NO 16
SEQ ID NO 16
SEQ ID NO 16
SED DATE: DATE: 1008
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CTHER INFORMATION: Description
CTHER INFORMATION: LINF-R2
US-09-898-234-16
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Pred. No.:
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                     OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
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                                                                  Length:
Matches:
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ORGANISM: Homo saptens
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ree: 2487.00 Matches: 455 reent Similarity: 100.00% Conservative: 0 st Local Similarity: 100.00% Mismatches: 0 sry Match: 100.00% Indels: 0 caps: 0 caps: 0 c9 Gaps: 0 c9-899-422A-2 (1-455) x US-09-898-234-16 (1-2141)	Oy 1 MetGlyLeuSerThrValProAspGeuLeuIeuValLeuGluLeuVal 20 1 HelfHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 	61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	ol Cyargelucyseluserelyserphermralasereluashilsbeukrghiscysleu 	Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120 110 111	Qy 121 ArgAspThrValCysGiyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140 	Oy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 	Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180 	Oy 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGinileGlu 200	Oy 201 ASNVALLYSGLYThrGluAspSerGlyThrThrValLeuLeuProLeuVall1ePhePhe 220	Oy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuWetTyrargTyrGlnArgTrpLys 240	Oy 241 SerLysLeuTyrSerlleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260 	Qy 261 GlyThrThrThrIvsProLeualaBroAsnProSerPheSerProThrProGlyPheThr 280 	Oy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300	1 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 	Oy 321 AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys 340

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NAME/KEY: CDS
LOCATION: (213)..(1580)
OTHER INFORMATION: LINF-R2
OTHER INFORMATION: LINF-R2
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## SERVERAL INNOVARATION:
## APPLICANT: Hampler, Adolph
## APPLICANT: Hamler, Adolph
## APPLICANT: Hamler, Adolph
## APPLICANT: Hamler, Adolph
## APPLICANT: Hamler, Adolph
## APPLICANT: Stratowa, Christian
## TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS
## TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS
## CURRENT APPLICATION TO HERE: 05/09/792,356
## CURRENT APPLICATION NUMBER: 08/477,639
## PRIOR PELING DATE: 1995-06-07
## PRIOR FILING DATE: 1995-06-07
## PRIOR FILING DATE: 1995-02-01
## PRIOR FILING DATE: 1993-11-17
## PRIOR APPLICATION NUMBER: 08/153,287
## PRIOR APPLICATION NUMBER: 07/511,430
## PRIOR FILING DATE: 1990-04-20
## NUMBER OF SEQ ID NOS: 87
## SOFTWARE: PATENTIN VOI 10 10
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Indels:
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Publication No. US20020183485A1
GENERAL INFORMATION:
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	RESULT 9 US-09-899-422-16 Sequence 16, Application US/09899422 Sequence 16, Application US/09899422 Patent No. US2002009656A1 GENERAL INFORMATION: APPLICANT: Haupmann, Rudolph APPLICANT: Haupmann, Rudolph APPLICANT: Maurer-Fogy, Ingrid APPLICANT: Stratowa, Christian TITLE OF INVENTION: The Receptors, TWF Binding Proteins and DNAs Coding for TITLE OF INVENTION: Them FILE REFERENCE: 98,385-H CURRENT APPLICATION NUMBER: US/09/899,422 CURRENT APPLICATION NUMBER: 09/525,998 PRIOR FILING DATE: 2000-03-15	FRIOR PEDILICATION NUMBER: 08/383,675 FRIOR PAPLICATION NUMBER: 08/153,287 FRIOR FILING DATE: 1995-02-01 FRIOR APPLICATION NUMBER: 08/153,287 FRIOR FILING DATE: 1993-11-17 FRIOR APPLICATION NUMBER: 07/821,750 FRIOR PEDILICATION NUMBER: 07/821,430 FRIOR FILING DATE: 1990-04-20 NUMBER OF SEQ ID NOS: 87 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: COS LENGTH: 2141 TYPE: DNA ORGANISM: Artificial Sequence FRAUDE: NAME/KEY: CDS LOCATION: (213). (1580) CTHER INFORMATION: 1TNF-R2 US-09-899-422-16	Alignment Scores: 1.14e-250 Length: 2141
	01 SercysSerlysCysArglysGluMetGlyGlnValGluIleSerSerCysThrValAsp	181 SerCysSerAsnCysLysLysSerLeuGluCysThrlysLeuCysLeuProGlnIleGlu 200	281 ProthreudlypheSerProValProSerSerThrPheThrSerSerBerThrTyrThr 300 1053 CCCACCCTGGGCTTCAGTCCCGTGCCCACTTCACTCTCTTTTTTTT

Qy 421 LeuGlyArgYalLeuArgAspNetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440	•	; APPLICANT: WALLACH, David ; BRAKEBUSCH, Cord ; TITLE OF INVENTION: TWF RECEPTOR ACTION MODULATION ; NTARER OF SPOITSWERS: 8	CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STRESSET: 419 Seventh Street, N.W.	CITT Washington STATE: D.C. COUNTRY: U.S. ZIP: 20004	;	CURRENT APPLICATION NUMBER: US/10/120, 997 FILING DATE: 12-Apr-2002	CLASSERICATION: <pre> CLASSERICATION: <pre> PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/054,970 FILING DATE: 03-MAY-1993 FILING DATE: 03-MAY-1993 } </pre></pre>	ATTOKNEY AGENT INFORMATION: REGISTRATION NUMBER: 34,033 REFERENCE/COCKET NUMBER: WALLACH-9	; TELECOMMONICATION: ; TELEPHONE: 202-68-5197 ; TELEPEAX: 202-737-3528 ; TELERX: 248633	; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: ; LENGTH: 2115 base pairs ; TYPE: nucleic acid	STRANBINESS: SIGIE ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA ; FEATURE:	; NAME/KEY: CDS ; LOCATION: 256.1620 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-120-397-1	1.17e-250 Length: 2487.00 Matches:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Dery Match: 100.00% Indels: 0 DB: 12 Gaps: 0	-09-899-422A-2 (1-455) x US-10-120-397-1 (1-2175)	Qy meta-yearserinratriosphenteurenrolenteurenteurenteurenval 20
OY 61 LyBCY8H18LyBGlyThrTyrLeuTyrAsnAspCy8ProGlyProGlyGlnAspThrAsp 80 Db 111111111111111111111111111111111111	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp [121 ArgasptnivalCysGlyCysArglysAsnClnTyrArgHisTyrTrpSerCluAsnLeu 140 	141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 	161 LysginasnthrvalcysthrcysHisalaglyPhePheLeuargGluasnGlucysVal 180 	181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200 	201 AsnVallysGlyThrGluAspSerGlyThrThrValLeuLeuVeuVroLeuValIlePhePhe 220	221 GlyLeucysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrargTyrGlnargTrpLys 240 	241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260 	261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280 	281 ProfhrLeuglyPheserProValProSerSerThrPheThrSerSerThrTyrThr 300 	301 ProGlyAspCysProAsnPheAlaalaProArgArgGluValAlaProProTyrGlnGly 320 	321 AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys 340 	341 TrpGluaspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360 	361 Alavalvalgluasnvalproproleuargfrplysgluphevalargargleuglyleu 380 		

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1516 CTGGGACGCGTGCTCCGCGACATGGACTGCTGGGCTGCCTGGAGGACATCGAGGAGGC 1575
                                   GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg
                                                           LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla
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TILLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
FILE REFERENCE: A-71992
CURRENT FILING DATE: 1902-09-24
PRIOR PELLING DATE: 1904-06-08
PRIOR PILING DATE: 1994-06-08
PRIOR PILING DATE: 1994-06-08
PRIOR PILING DATE: 1994-06-08
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PRIOR PILING DATE: 1994-06-08
PRIOR PILING DATE: 1994-06-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-11
SPIOR PILING DATE: 1999-09-11
PRIOR PILING DATE: 1999-09-11
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SEQ ID NO 3
LENGHH: 1368
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LOCATION: (1)..(1365)
OTHER INFORMATION:
FEATURE:
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; LOCATION: (1)..(120)
; OTHER INFORMATION:
US-10-252-408-3
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LOCATION: (121). ()
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
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GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAAGAGA 375
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                                                                     PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
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Sequence 11, Application US/09898234

Patent No. US20020155112A1

GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph

APPLICANT: Hammler, Adolph

APPLICANT: Hammler, Adolph

APPLICANT: Mamer-Fogy, Ingrid

APPLICANTON: Them

TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

FILE REFERENCE: 2001-07-03

CURRENT APPLICATION NUMBER: 08/383,676

PRIOR FILING DATE: 1993-01-07

PRIOR FILING DATE: 1993-11-17

PRIOR FILING DATE: 1993-11-17

PRIOR FILING DATE: 1992-01-02

PRIOR FILING DATE: 1992-01-02

PRIOR FILING DATE: 1992-01-02

PRIOR FILING DATE: 1990-04-20

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
                                                  LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
           GlylleTyrProSerGlyVallleGlyLeuValProHisLeuGlyAspArgGluLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr
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COTHER INFORMATION: Description of Artificial Sequence: CDNA insert of COTHER INFORMATION: LambdaTNF-BP15 and pINF-BP15 vectors
US-09-898-234-11
                                                                                                       LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
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Matches:
Conservative:
Mismatches:
Indels:
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2069.00
100.00%
100.00%
83.19%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                             US-09-898-234-11
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1334
                                                                     1261
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                   GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys
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                                                            LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
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OTHER INFORMATION: Description of Artificial Sequence: o
OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
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Matches:
Conservative:
Mismatches:
Indels:
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FILE OF INVENTION: Them
FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 2001-08-17
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-02-11
PRIOR PILING DATE: 1991-11-17
PRIOR PILING DATE: 1991-11-17
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SENTARE: 1334
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Best Local Similarity:
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LOCATION: (21
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APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: INF Receptors, TNF Binding Proteins and DNAs Coding for
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                                                                                              AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe
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Patent No. US20020090676A1

GENERAL INFORMATION:
APPLICANT: Hummler, Adolph
APPLICANT: Hummler, Adolph
APPLICANT: Stratcwa, Christian
TITLE OF INVENTION: TWE Receptors, TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-H
CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 1993-11-17
PRIOR PILING DATE: 1993-11-17
PRIOR PILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-04-02
PRIOR FILING DATE: 1993-04-02
PRIOR FILING DATE: 1993-04-02
PRIOR FILING DATE: 1990-04-06
PRIOR FILING DATE: 1990-04-06
PRIOR FILING DATE: 1990-04-20
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SOFTWARE: Patentin Ver. 2.0
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LENGTH: 1334
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LOCATION: (213)..(1325)
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CDNA insert
Description of Artificial Sequence: ( lambdaINF-BP15 and pINF-BP15 vectors
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Mismatches:
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Matches:
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US-09-899-422-11
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Query Match:
                                Alignment Scores:
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Qy 301 ProGlyAspCysProAsnPheAlaAlaAlaProArgArgGluValAlaProProTyrGlnGly 320 bb	SULT 15 SULT 15 Sequence 21 Se	Db 213 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGTGTTCCTGGAGCTGTTGGTG 272 Qy 21 GlylleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLy8Arg 40

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